

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:50:38 ; Search time 22 Seconds  
(without alignments)  
2801.007 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 641

Sequence: 1 MAKAAIGIDLGTTSCVGV.....FGAGPKGSGSGPTIREVD 641

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	641	100.0	641	2	A45871	dnak-type molecule
2	412	64.3	640	2	A29160	dnak-type molecule
3	370	57.7	641	2	S53357	dnak-type molecule
4	209	32.6	641	2	S35718	dnak-type molecule
5	175	27.3	638	2	S31766	dnak-type molecule
6	114	17.8	641	2	I54542	dnak-type molecule
7	101	15.8	642	2	JH0095	dnak-type molecule
8	80	12.5	420	2	A26283	dnak-type molecule
9	65	10.1	65	2	I79540	dnak-type molecule
10	55	8.6	633	2	S08211	dnak-type molecule
11	55	8.6	633	2	S10859	dnak-type molecule
12	55	8.6	634	2	A25646	dnak-type molecule
13	55	8.6	639	2	A55719	dnak-type molecule
14	55	8.6	641	2	I49761	dnak-type molecule
15	55	8.6	641	2	S41415	dnak-type molecule
16	55	8.6	641	2	B45871	dnak-type molecule
17	54	8.4	640	2	T43724	dnak-type molecule
18	53	8.3	646	2	S07197	dnak-type molecule
19	53	8.3	646	2	A35922	dnak-type molecule
20	53	8.3	646	2	JC4853	dnak-type molecule
21	53	8.3	646	2	A27077	dnak-type molecule
22	53	8.3	646	2	S31716	dnak-type molecule
23	53	8.3	646	2	A45935	dnak-type molecule
24	53	8.3	647	1	HXL70	dnak-type molecule
25	53	8.3	650	2	S11456	dnak-type molecule
26	53	8.3	651	2	A36333	dnak-type molecule
27	50	7.8	372	2	P00138	dnak-type molecule
28	48	7.5	646	2	B86295	hypothetical prote
29	47	7.3	125	2	I37564	dnak-type molecule

30	47	7.3	643	2	S09036	dnak-type molecule
31	45	7.0	636	2	T45468	dnak-type molecule
32	44	6.9	654	2	S27004	dnak-type molecule
33	43	6.7	645	2	I51129	dnak-type molecule
34	42	6.6	379	2	I46588	dnak-type molecule
35	42	6.6	617	2	H96605	probable heat shoc
36	42	6.6	643	2	S25585	dnak-type molecule
37	42	6.6	653	2	T48270	dnak-type molecule
38	41	6.4	637	2	A48469	dnak-type molecule
39	39	6.1	278	2	I51344	dnak-type molecule
40	39	6.1	640	2	T43730	dnak-type molecule
41	39	6.1	650	2	JC7088	heat shock protein
42	39	6.1	651	2	S21175	dnak-type molecule
43	38	5.9	68	2	B03309	dnak-type molecule
44	38	5.9	214	2	A03309	dnak-type molecule
45	38	5.9	640	1	HHRW7A	dnak-type molecule

#### ALIGNMENTS

##### RESULT 1

A45871

dnak-type molecular chaperone HSP70-1 - human

N:Alternate names: heat shock protein HSP70-1

C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 20-Aug-1999

C:Accession: A45871

R:Milner, C.M.; Campbell, R.D.

Immunogenetics 32, 242-251, 1990

A:Title: Structure and expression of the three MHC-linked HSP70 genes.

A:Reference number: A45871; MUID:91055806; PMID:1700760

A:Accession: A45871

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-641 <MIL>

A:Cross-references: GB:M59828; GB:M34267; NID:q188487; PIDN:AAA63226.1; PID:q188488;

C:Function: Involved in protein folding and assembling/disassembling of protein co

A:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match	Score	641:	DB 2:	Length	641:
Best Local Similarity	100.0%				
Matches	641;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
QY	1	MAKAAIGIDIGTTCYGVFOHGKVELIANDOGKRTTPSYAFTDRLIGDAKNQVA	60		
DB	1	MAKAAIGIDIGTTCYGVFOHGKVELIANDOGKRTTPSYAFTDRLIGDAKNQVA	60		
QY	61	LNPOVTVDARLIGRKFGDPVQSDMKHWPQVINDGKRPVQVSYKGETKAFYPEEIS	120		
DB	61	LNPOVTVDARLIGRKFGDPVQSDMKHWPQVINDGKRPVQVSYKGETKAFYPEEIS	120		
QY	121	SMVLTKMKEIAEAYIGYVTAATVTPRAYFNDISOQAKTKDAGVAGLWVLRINPTFAA	180		
DB	121	SMVLTKMKEIAEAYIGYVTAATVTPRAYFNDISOQAKTKDAGVAGLWVLRINPTFAA	180		
QY	181	IAYGLDRFGKERNLIFDLGGTFDVSILITIDGIFPVKAVAGPTHTLGGEDFDRLVNH	240		
DB	181	IAYGLDRFGKERNLIFDLGGTFDVSILITIDGIFPVKAVAGPTHTLGGEDFDRLVNH	240		
QY	241	FVEEFKRRHKDISONKRAVRRLRTACERAKRTSSQASLEIDSLEFEGIDFYTSTR	300		
DB	241	FVEEFKRRHKDISONKRAVRRLRTACERAKRTSSQASLEIDSLEFEGIDFYTSTR	300		
QY	301	RPEELCSDFRSTLEPVRKALROAKLDAQYHDLVYVGGSTRIPVQKLLDDFFGRPLN	360		
DB	301	RPEELCSDFRSTLEPVRKALROAKLDAQYHDLVYVGGSTRIPVQKLLDDFFGRPLN	360		
QY	361	KSINDEAVVGAQAQVAILMGDKSENQODLLLDVAPLSIGLETAGVMTALIKRNSTI	420		
DB	361	KSINDEAVVGAQAQVAILMGDKSENQODLLLDVAPLSIGLETAGVMTALIKRNSTI	420		

```

QY      421 PKRQOIFETTSNDOPGVILIOYEGERAMTKNNLTGPELSCIPPARGPQIIEVFDI    480
         |||||||
Db       421 PPKQOIIFTTYSNDOGCVLILOVEERAMTKDNLTLGRFELSGLTPPARGPOILEVTDI   480
QY      481 DANGILMTATDKSTGGKAKKITITTDKGRLSKKEELIERVOEAEKYKADEYOERVSASN  540
         |||||||
Db       481 DANGILTAVATOKSGTGKANIKITITNDKGRLSKEELIERVOEAEKYKADEVOREVSASN  540
QY      541 ALESAFAFNKKSAVEDEGLKGISEADKKKVLDKCCEVISWMDANTLARLKDEFENHRRKLE 600
         |||||||
Db       541 ALESAFAFNKKSAFEDEGLKGISEADKKVKDCCEVISWDANLAELAEDFEHNHRKLE     600
QY      601 QVCNPFIISGLYGAGPGGFAGCPKGSNGSSGTPIEEVD 641
         |||||||
Db       601 QVCNPFIIISGLYGAGPGFGGFGAQPCKGSSGSTPIIEVD 641

RESULT 2
A29160
dnak-type molecular chaperone HSPAL1 - human
M.Alternate names: heat shock protein, 70k
C.Species: Homo sapiens (man)
C.Date: 16-Aug-1988 #sequence_revision 02-Jul-1996 #text-change 20-Aug-1999
C.Accession: A29160; I37561; I37562
R.Hunt, C.; Morimoto, R.I.
Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985
A.Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the nu...
A.Reference number: A29160; MUID:86016721; PMID:3931075
A.Accession: A29160
A.Molecule type: DNA
A.Residues: 1-640 <HD>X
A.Cross-references: GB:M1171; GB:M15432; NID:g184416; PIDN:AAA52697.1; PID:g386785
A.Note: The authors mistranslated residues 463, 491, and 492
R.Drabent, B., Genthe, A.; Benecke, B.J.
Nucleic Acids Res. 14, 8933-8948, 1986
A>Title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepared f...
A.Reference number: I37561; MUID:87066768; PMID:3786141
A.Accession: I37561
A.Status: translation not shown; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 616-640 <RE2>
A.Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483
C.Genetics:
A.Gene: GDB:HSPA1L; HSP70-HOM
A.Cross-references: GDB:I20058; OMIM:140559
A.Map position: 6p21.3-6p21.3
A.Introns : #status absent
C.Function:
A.Description: involved in protein folding and assembling/disassembling of protein compo...
C.Subfamily: heat shock protein 70
C.Keywords: ATP; molecular chaperone

Query Match          64.3%; Score 412; Db 2; Length 640;
Best Local Similarity 99.7%; Pred.No.0;
Matches 632; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

OY	188	TGKRRNLVLDLGGCTFVSLITIDGIFEVKATDAGTTHLGGEDPNRLVNHVEEFKR	247
Db	188	TGKRRNLVLDLGGCTFVSLITIDGIFEVKATDAGTTHLGGEDPNRLVNHVEEFKR	247
OY	248	KHKRDISONKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSTITRAFEEELCS	307
Db	248	KHKRDISONKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSTITRAFEEELCS	307
OY	308	DLFRSTLEPVEKALRDALDKAQIHDVLVYGGSTRIRKVKQLLODFNGRDLNKSINPDE	367
Db	308	DLFRSTLEPVEKALRDALDKAQIHDVLVYGGSTRIRKVKQLLODFNGRDLNKSINPDE	367
OY	368	AVAYAAVAOAAIIMDKSENVODLLLDVAPLSGLETAGVMTALLKRNSTIPTKTQOI	427
Db	368	AVGYCAAOAAIIMDKSENVODLLLDVAPLSGLETAGVMTALLKRNSTIPTKTQOI	427
OY	428	FTTYSDNQPGVLIQYEGSERAMTKDNMLLGFEEISGIPPADRGVQIETVTFDDANGILN	487
Db	428	FTTYSDNQPGVLIQYEGSERAMTKDNMLLGFEEISGIPPADRGVQIETVTFDDANGILN	486
OY	488	VTAITKSTGKANKITITNDKGRSLKEEIERVVOAEKTKADDEVQRRVSKNNLESYAF	547
Db	487	VTAITKSTGKANKITITNDKGRSLKEEIERVVOAEKTKADDEVQRRVSKNNLESYAF	546
OY	548	NMKSAYDEGLKGIISEADKKRVLDKCEVTSWLDANTIAEKDEFEHKRKELEOVCAPII	607
Db	547	NMKSAYDEGLKGIISEADKKRVLDKCEVTSWLDANTIAEKDEFEHKRKELEOVCAPII	606
OY	608	SGLYOGAGPGPGGFGAOGPKGSGSGSPITIEVD	641
Db	607	SGLYOGAGPGPGGFGAOGPKGSGSGSPITIEVD	640

RESULT 3

S53357

dnak-t type molecular chapetone hsp70 - bovine

N:Alternate names: 70K heat shock protein

C:Species: Bos primigenius taurus (cattle)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jul-2000

C:Accession: S53357

R:Gutierrez, J.A.; Guerriero Jr., V.

Biochem. J. 305, 197-203, 1995

A:Title: Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-

A:Reference number: S53357; MUID:95126904; PMID:7826329

A:Accession: S53357

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-641 <GDU>

A:Cross-references: EMBL:U09861; NID:9497937; PIDN:AAA73914.1; PID:9497938

C:Genetics:

A:Gene: hsp70

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chapetone

Query Match

Best Local Similarity 57.7%; Score 370; DB 2; Length 641;

Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	138	PVTNAVITVPAYFENDSQOATKDAGVLAGLVLRLINEPTAAAIAYGLDRTGKGERNVLI	197
Db	138	PVTNAVITVPAYFENDSQOATKDAGVLAGLVLRLINEPTAAAIAYGLDRTGKGERNVLI	197
OY	198	FDLGGCTFVSLITIDGIFEVKATAGTTHLGGEDFDRNLVNHVEEFKRRKKHKDKIQNK	257
Db	198	FDLGGCTFVSLITIDGIFEVKATAGTTHLGGEDFDRNLVNHVEEFKRRKKHKDKIQNK	257
OY	258	RAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSTITRAFEEELCSDLFRSTLEPV	317
Db	258	RAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSTITRAFEEELCSDLFRSTLEPV	317

Qy	318	EK.RBDAKLDKAO.IHDI.VIVNGSRR.IPKYOK.LLODPFNGSDLKSI.NPDEAAYGGAOA	377
Db	318	EKALDLADLDAQ.IHDI.VLVGSGRR.IPKYOK.LLODPFNGSDLKSI.NPDEAAYGGAOA	377
Qy	378	AILMGDKSENVOD.LLLDVAP.PLSIGLETAGVMTALIKRNSI.IPTKQTO.IFTTYYSDNOG	437
Db	378	AILMGDKSENVOD.LLLDVAP.PLSIGLETAGVMTALIKRNSI.IPTKQTO.IFTTYYSDNOG	437
Qy	438	VLIQVYBGERAMT.DNNLLGRFEL.SGTPPAPRGVPO.IEYTFDDANGILNVATIDKSTGK	497
Db	438	VLIQVYBGERAMT.DNNLLGRFEL.SGTPPAPRGVPO.IEYTFDDANGILNVATIDKSTGK	497
Qy	498	ANKITITNDKGR.LSKEETIERVAVO.EAEYKKA.EDEVQERERVSANKNALESYAFNMKS.AVEDEG	557
Db	498	ANKITITNDKGR.LSKEETIERVAVO.EAEYKKA.EDEVQERERVSANKNALESYAFNMKS.AVEDEG	557
Qy	558	LKGRISSEADKKVYLDKQCEVYSWIDANTATLAKDPEEHIKRRELEQVYCNPIIS	608
Db	558	LKGRISSEADKKVYLDKQCEVYSWIDANTATLAKDPEEHIKRRELEQVYCNPIIS	608

RESULT 4  
S35718  
dnak-type molecular chaperone hsp70 - pig  
N:Alternate names: heat shock protein hsp70  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 09-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S35718  
R:Peelman, L.J.; van de Weghe, A.R.; Coppieters, W.R.; Van Zeveren, A.J.; Bouquet, Y.H.  
Immunogenetics 35, 286-289, 1992  
A:title: Complete nucleotide sequence of a porcine HSP70 gene.  
A:Accession number: S35718; MUID:92175874; PMID:1339404  
A:Accession: S35718  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-641 <PER>  
A:Cross-references: EMBL:M69100  
C:Genetics:  
A:Gene: hsp70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP, molecular chaperone

Query Match	32.6%	Score	20.9	DB 2:	Length	641	
Best Local Similarity	99.7%	Pred.	No. 1.6e-205				
Matches	309	Conservative	0	Mismatches	1	Indels	0
						Gaps	0
QY	141	NAVIVPAPVAFNDSQOARKDAGVIAGLWVLRILNPTAAIAYAGDRKGCERNLIFDL	200				
DB	141	NAVIVPAPVAFNDSQOARKDAGVIAGLWVLRILNPTAAIAYAGDRKGCERNLIFDL	200				
QY	201	GGGTDFVSLITLIDGIFFEYKATAGDTHLGGEDFNRLVNHFEERKRRKKKDISONKRAY	260				
DB	201	GGGTDFVSLITLIDGIFFEYKATAGDTHLGGEDFNRLVNHFEERKRRKKKDISONKRAY	260				
QY	261	RRLRFACERAKRTLSSSTQASLEIDSLFEGIDFYYSITRAPREELCSDLFRSLPEPVEKA	320				
DB	261	RRLRFACERAKRTLSSSTQASLEIDSLFEGIDFYYSITRAPREELCSDLFRSLPEPVEKA	320				
QY	321	LEDATLDRKAQIHDLVVGSGSTRIPVOKLLODFNGRDLNKSINPDEAVAYAAVQAAIL	380				
DB	321	LEDATLDRKAQIHDLVVGSGSTRIPVOKLLODFNGRDLNKSINPDEAVAYAAVQAAIL	380				
QY	381	MGDKSENVODLLDLDPVAPLSLGLETAGGVMAILIKRNSTIPPKQOIFVYSDNPGVILI	440				
DB	381	MGDKSENVODLLDLDPVAPLSLGLETAGGVMAILIKRNSTIPPKQOIFVYSDNPGVILI	440				
QY	441	OYVEGERAMT 450					
DB	441	OYVEGERAMT 450					

RESULT 5  
S31766  
dnaK-type molecular chaperone hsp70 - green monkey  
N.Alternate names: heat shock protein 70  
C.Species: Cercopithecus aethiops (green monkey, grivet)  
C.Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C.Accession: S31766; 136927  
R.Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
submitted to the EMBL Data Library, January 1993  
A.Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock prot  
A.Reference number: S31766  
A.Accession: S31766  
A.Molecule type: mRNA  
A.Residues: 1-638 <SAI>  
R.Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
FEBS Lett. 355, 282-286, 1994  
A.Title: The hsc70 gene, which is slightly induced by heat is the main virus inducible  
A.Reference number: 136927; MUID:95080396; PMID:7968690  
A.Accession: 136927  
A.Status: Preliminary; translated from GB/EMBL/DBD  
A.Molecule type: mRNA  
A.Residues: 1-638 <RES>  
A.Cross-references: EMBL:X70684; NID:922781; PIDN:CAAS0019.1; PID:922782  
A.Experimental source: Kidney; cell line COS-1  
C.Genetics:  
A.Gene: hsp70  
C.Function:  
A.Description: involved in protein folding and assembling/disassembling of protein co  
C.Superfamily: heat shock protein 70  
C.Keywords: ATP; molecular chaperone

Query Match	27.3%	Score 175;	DB 2;	length 638;
Best Local Similarity	100.0%	Pred. No. 1.2e-170;		
Matches 175;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	231	EDFDNRILVHFEFEERKRHKKD	ISONKRAVRRLTRACERAKRTLSSTQASLEIDSP	290
DB	229	EDFDNRILVHFEFEERKRHKKD	ISONKRAVRRLTRACERAKRTLSSTQASLEIDSP	288
QY	291	IDFYVSTTRAFPEELCSDL	FRSTLEPVEKALIDAKLDAQIHDVLVVGSTRIPVKQL	350
DB	289	IDFYVSTTRAFPEELCSDL	FRSTLEPVEKALIDAKLDAQIHDVLVVGSTRIPVKQL	348
QY	351	QDFEFGRIIDNKSINPDEA	VAAGAAVOAALILMGDKSENNODLLLLDVAPLSIGLEF	405
DB	349	QDFEFGRIIDNKSINPDEA	VAAGAAVOAALILMGDKSENNODLLLDVAPLSIGLEF	403

RESULT 6  
I54542  
dnaK-type molecular chaperone HSP70 - rat  
N.Alternate names: dnaK-type molecular chaperone HSP70ib; heat shock protein 70  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text change 08-Dec-2000  
C.Accession: I54542; I68986; S43388; S47522; I55574; S35955; S38199; S41413; S41414  
R.Walter, L.; Rautn, F.; Gunther, E.  
Immunogenetics 40, 325-330, 1994  
A.Title: Comparative analysis of the three major histocompatibility complex-linked heat  
A.Reference number: I54542; MUID:95012453; PMID:7927536  
A.Accession: I54542  
A.Status: preliminary; translated from GR/EMBL/DBDJB  
A.Molecule type: DNA  
A.Residues: 1-641 <MAL1>  
A.Cross-references: EMBL.X77207; NID:g1814000; PIDN:CAA5442.1; PID:g450930  
A.Experimental source: HSP70.1  
A.Genetics: HSP1  
A.Accession: I68986  
A.Status: preliminary; translated from GR/EMBL/DBDJB  
A.Molecule type: DNA  
A.Residues: 1-641 <MAL2>  
A.Cross-references: EMBL.X77208; NID:g927512; PIDN:CAA54423.1; PID:g450932  
A.Experimental source: HSP70.2  
A.Genetics: HSP2

R.Mestrlil, R.; Chl, S.H.; Sayen, M.R.; Dillmann, W.H.  
Biochem. J. 298, 561-569, 1994  
A:Title: Isolation of a novel inducible rat heat-shock protein (hsp70) gene and its expr  
A:Reference number: 543388; MUID:94190258; PMID:8141767  
A:Accession: 543388  
A:Molecule type: DNA  
A:Residues: 1-70, 'NG', 73-109, 'K', 111-203, 'R', 205-261, 'P', 263, 'ADGV', 268-641 <MRS>  
A:Cross-references: EMBL:X75357; NID:9407163; PIDN:CAA53140.1; PID:9407164  
A:Experimental source: Ischaemic rat heart  
R:Lowy, D.G.; Widal, W.; Krawczyk, Z.; Wolniczek, P.; Wisniewski, J.  
Biochim. Biophys. Acta 1219, 64-72, 1994  
A:Title: Cloning, nucleotide sequence and expression of rat heat inducible hsp70 gene.  
A:Reference number: 547522; MUID:94368874; PMID:8086479  
A:Accession: 547522  
A:Molecule type: DNA  
A:Residues: 1-70, 'NG', 73-407, 'A', 409-641 <LIS>  
A:Cross-references: EMBL:X74271; NID:9413498; PIDN:CAA52328.1; PID:9396270  
A:Note: The authors translated the codon CCG for residue 365 as Asp  
J. Neurosci. Res. 36, 325-335, 1993  
A:Title: cDNA cloning and expression of stress-inducible rat hsp70 in normal and injured  
A:Reference number: 156574; MUID:94096443; PMID:8271311  
A:Accession: 156574  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-226, 'D', 228-641 <LON>  
A:Cross-references: GB:LI6764; NID:9294567; PIDN:AAA17441.1; PID:9294568  
A:Genetics: <HSP1>  
A:Gene: hsp70.1  
C:Genetics: <HSP2>  
A:Gene: hsp70.2  
C:Function:  
A:Description: Involved in protein folding and assembling/dissassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 17.8%; Score 114; DB 2; Length 641;  
Best Local Similarity 100.0%; Pred. No. 4.6e-108;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 TLEPVEKALRDALDKAQLHDVLVVGSTRIPKVKLLDFFNGRLNKSINDEAVAG 372  
DB 313 TLEPVEKALRDALDKAQLHDVLVVGSTRIPKVKLLDFFNGRLNKSINDEAVAG 372  
QY 373 AAVQAAILMGDKSENVDLLDVAPLSLGLETAGVMTALIKRNSTIPTKQTQ 426  
DB 373 AAVQAAILMGDKSENVDLLDVAPLSLGLETAGVMTALIKRNSTIPTKQTQ 426

RESULT 7  
JH0095  
dnak-type molecular chaperone hsp70 - mouse  
N:Alternate names: heat shock protein 70  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Aug-1999  
C:Accession: JH0095  
R:Hunt, C.; Calderwood, S.  
Gene 87, 199-204, 1990  
A:Title: Characterization and sequence of a mouse hsp70 gene and its expression in mouse  
A:Reference number: JH0095; MUID:90236310; PMID:2332169  
A:Accession: JH0095  
A:Molecule type: DNA  
A:Residues: 1-642 <HUN>  
A:Cross-references: GB:M35021; NID:9194022; PIDN:AAA37864.1; PID:9387211  
A:Experimental source: strain AJ  
C:Function:  
A:Description: Involved in protein folding and assembling/dissassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 15.8%; Score 101; DB 2; Length 642;  
Best Local Similarity 100.0%; Pred. No. 9.9e-95;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 PVTNAVITVPAYFENDSORQATKDAGIAGLVNLRITNEPTAAAIYGLDRGKGERNVLI 197  
DB 138 PVTNAVITVPAYFENDSORQATKDAGIAGLVNLRITNEPTAAAIYGLDRGKGERNVLI 197  
QY 198 FDLGGTEFVSLITLTDGIFEFKATAGDTHLGGEPDNRV 238  
DB 198 FDLGGTEFVSLITLTDGIFEFKATAGDTHLGGEPDNRV 238

RESULT 8  
A26283  
dnak-type molecular chaperone - mouse (fragment)  
N:Alternate names: heat shock protein 68  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A26283  
R:Lowy, D.G.; Moran, L.A.  
J. Biol. Chem. 261, 2102-2112, 1986  
A:Title: Molecular cloning and analysis of DNA complementary to three mouse Mr-68,000  
A:Reference number: A26283; MUID:86111900; PMID:2868009  
A:Accession: A26283  
A:Molecule type: mRNA  
A:Residues: 1-420 <LON>  
A:Cross-references: GB:M12571; NID:9194014; PIDN:AAA57234.1; PID:9387208  
A:Note: The authors translated the codon CTG for residue 173 as Val and CGC for resid  
C:Function:  
A:Description: Involved in protein folding and assembling/dissassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 12.5%; Score 80; DB 2; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2.4e-73;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 DLVVGSTRIPKVKLLDFFNGRLNKSINDEAVAGAQAAILMGDKSENVDLL 392  
DB 112 DLVVGSTRIPKVKLLDFFNGRLNKSINDEAVAGAQAAILMGDKSENVDLL 171  
QY 393 LLDVAPLSGLETAGVMTA 412  
DB 172 LLDVAPLSGLETAGVMTA 191

RESULT 9  
I79540  
dnak-type molecular chaperone HSP70-2 - human (fragment)  
N:Alternate names: Chaperonin HSP70-2; MHC heat shock protein HSP70-2  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 20-Aug-1999  
C:Accession: I79540  
R:Sargent, C.A.; Dunham, I.; Trowsdale, J.; Campbell, R.D.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1968-1972, 1989  
A:Title: Human major histocompatibility complex contains genes for the major heat sho  
A:Reference number: I59139; MUID:89184548; PMID:2538825  
A:Accession: I79540  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-65 <RHS>  
A:Cross-references: GB:M24744; NID:9188529; PIDN:AAA59845.1; PID:9188530  
C:Genetics:  
A:Gene: HSP70-2  
C:Function:  
A:Description: Involved in protein folding and assembling/dissassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 10.1%; Score 65; DB 2; Length 65;  
Best Local Similarity 100.0%; Pred. No. 1.1e-58;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 NKSINDEAVAGAQAAILMGDKSENVDLLDVAPLSLGLETAGVMTALIKRNST 419  
I79540

Db 1 NKSINPEAVAGAAVQAAIIMGDKSENVDLLILDVAPLSLGLETAGVMTALIKRNST 60  
 Oy 420 IPTKO 424  
 Db 61 IPTKO 65

## RESULT 10

S08211  
 dnak-type molecular chaperone hsc70 - rat  
 N:Alternate names: heat shock protein 70.2; heat shock protein, testis-specific  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 30-Jan-1998  
 C:Accession: S08211  
 R:Wisniewski, J.; Kordula, T.; Krawczyk, Z.  
 Biochim. Biophys. Acta 1048, 93-99, 1990  
 A:Title: Isolation and nucleotide sequence analysis of the rat testis-specific major heat shock protein  
 A:Reference number: S08211; MUID:90122930; PMID:1688714  
 A:Accession: S08211  
 A:Molecule type: DNA  
 A:Residues: 1-633 <WIS>  
 A:Cross-references: EMBL:X15705  
 A:Note: the authors translated the codon GAG for residue 217 as Asp  
 C:Genetics:  
 A:Gene: hsc70  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 8.6%; Score 55; DB 2; Length 633;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AIGIDLTGTTSCVGVFGHGKVEIIANDGNNRTTSPYVAFDTERLIGDAKNOVA 60  
 Db 7 AIGIDLTGTTSCVGVFGHGKVEIIANDGNNRTTSPYVAFDTERLIGDAKNOVA 61

## RESULT 11

S10859  
 dnak-type molecular chaperone HSP70.2 - mouse  
 N:Alternate names: heat shock protein 70.2  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 30-Jan-1998  
 C:Accession: S10859  
 R:Zakeri, Z.F.; Wolgemuth, D.J.; Hunt, C.R.  
 Mol. Cell. Biol. 8, 2925-2932, 1988  
 A:Title: Identification and sequence analysis of a new member of the mouse HSP70 gene fa  
 A:Reference number: S10859; MUID:88302212; PMID:3405224  
 A:Accession: S10859  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-633 <ZAK>  
 A:Cross-references: EMBL:M20567  
 C:Genetics:  
 A:Gene: HSP70.2  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 8.6%; Score 55; DB 2; Length 633;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AIGIDLTGTTSCVGVFGHGKVEIIANDGNNRTTSPYVAFDTERLIGDAKNOVA 60  
 Db 7 AIGIDLTGTTSCVGVFGHGKVEIIANDGNNRTTSPYVAFDTERLIGDAKNOVA 61

## RESULT 12

A25646  
 dnak-type molecular chaperone - chicken  
 N:Alternate names: heat shock protein 70  
 C:Species: Gallus gallus (chicken)  
 C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
 C:Accession: A25646  
 R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.  
 J. Biol. Chem. 261, 12692-12699, 1986  
 A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 ge  
 A:Reference number: A25646; MUID:86304452; PMID:3017985  
 A:Accession: A25646  
 A:Molecule type: DNA  
 A:Residues: 1-634 <MOR>  
 A:Cross-references: GB:J02579; NID:q211940; PIDN:AAA48825.1; PID:q211941  
 A:Note: the authors translated the codon TCG for residue 583 as Trp  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 8.6%; Score 55; DB 2; Length 634;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AIGIDLTGTTSCVGVFGHGKVEIIANDGNNRTTSPYVAFDTERLIGDAKNOVA 60  
 Db 7 AIGIDLTGTTSCVGVFGHGKVEIIANDGNNRTTSPYVAFDTERLIGDAKNOVA 61

## RESULT 13

A55719  
 dnak-type molecular chaperone HSPA2 - human  
 N:Alternate names: heat shock protein A2  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 20-Aug-1999  
 C:Accession: A55719  
 R:Bonnycastle, L.L.C.; Yu, C.E.; Hunt, C.R.; Trask, B.J.; Clancy, K.P.; Weber, J.L.;  
 Genomics 23, 85-93, 1994  
 A:Title: Cloning, sequencing, and mapping of the human chromosome 14 heat shock prote  
 A:Reference number: A55719; MUID:95130116; PMID:7829106  
 A:Accession: A55719  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-639 <BON>  
 A:Cross-references: GB:L26336; NID:q476704; PIDN:AAA52698.1; PID:q476705  
 C:Genetics:  
 A:Gene: GDB:HSPA2  
 A:Cross-references: GDB:120059; OMIM:140560  
 A:Map position: 14q22-14q22  
 A:Introns: #status absent  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 8.6%; Score 55; DB 2; Length 639;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AIGIDLTGTTSCVGVFGHGKVEIIANDGNNRTTSPYVAFDTERLIGDAKNOVA 60  
 Db 7 AIGIDLTGTTSCVGVFGHGKVEIIANDGNNRTTSPYVAFDTERLIGDAKNOVA 61

## RESULT 14

I49761  
 dnak-type molecular chaperone Hsc70b - mouse  
 N:Alternate names: heat shock protein 70  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
 C:Accession: I49761  
 R:Snook, M.; Olavsen, M.G.; Van Vugt, H.; Milner, C.M.; Teuscher, C.; Campbell, R.D.  
 Immunogenetics 40, 159-162, 1994

A>Title: Coding sequences and levels of expression of Hsc70t are identical in mice with  
A:Reference number: 149761; MUID:9429288; PMID:8026864  
A:Accession: 149761  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-641 <RES>  
A:Cross-references: GB:L27086; NID:9457299; PIDN:AAA59362.1; PID:9457300  
C:Genetics:  
A:Gene: Hsc70t  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 8.6%; Score 55; DB 2; Length 641;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AIGIDGTTYSCVGFQHGKVELIANDGNNRTTPSYAFTDTERLIGDAKNOVA 60  
|||||  
DB 8 AIGIDGTTYSCVGFQHGKVELIANDGNNRTTPSYAFTDTERLIGDAKNOVA 62  
|||||

RESULT 15  
.S41415  
dnaK-type molecular chaperone Hsp70.3 - rat  
N:Alternate names: heat shock protein 70  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jul-2000  
C:Accession: S41415; 168967  
R:Lutz, W.  
submitted to the EMBL Data Library, January 1994  
A:Reference number: S41413  
A:Accession: S41415  
A:Molecule type: DNA  
A:Residues: 1-641 <LUT>  
A:Cross-references: EMBL:X77209; NID:91814002; PIDN:CAA54424.1; PID:9450934  
R:Walter, L.; Rauh, F.; Gunther, E.  
Immunogenetics 40, 325-330, 1994  
A>Title: Comparative analysis of the three major histocompatibility complex-linked heat  
A:Reference number: 154542; MUID:95012453; PMID:7927536  
A:Accession: 168987  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-641 <RES>  
A:Cross-references: EMBL:X77209; NID:91814002; PIDN:CAA54424.1; PID:9450934  
C:Genetics:  
A:Gene: Hsp70-3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 8.6%; Score 55; DB 2; Length 641;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AIGIDGTTYSCVGFQHGKVELIANDGNNRTTPSYAFTDTERLIGDAKNOVA 60  
|||||  
DB 8 AIGIDGTTYSCVGFQHGKVELIANDGNNRTTPSYAFTDTERLIGDAKNOVA 62  
|||||

Search completed: December 4, 2002, 16:53:11  
Job time : 23 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:42:22 : Search time 12 Seconds  
(without alignments)  
867.610 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 3263

Sequence: 1 MAKAAAGIDLGTTSCVGV.....FGAGPKGSGSGPTIEVD 641

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA:\*  
1: /cgn2\_6/ptodata/1/pubppa/US08\_NEM\_PUB pep:\*  
2: /cgn2\_6/ptodata/1/pubppa/PCIT\_NEM\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEM\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB pep:\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEM\_PUB pep:\*  
6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB pep:\*  
7: /cgn2\_6/ptodata/1/pubppa/PCITUS\_PUBCOMB pep:\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB pep:\*  
9: /cgn2\_6/ptodata/1/pubppa/US09\_NEM\_PUB pep:\*  
10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB pep:\*  
11: /cgn2\_6/ptodata/1/pubppa/US10\_NEM\_PUB pep:\*  
12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB pep:\*  
13: /cgn2\_6/ptodata/1/pubppa/US60\_NEM\_PUB pep:\*  
14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3263	100.0	641	10	US-09-759-010-3
2	3125.5	95.8	642	10	US-09-761-534A-10
3	2859.5	87.6	646	9	US-08-870-759-43
4	2859.5	87.6	646	10	US-09-759-010-4
5	2740	84.0	665	10	US-09-925-302-724
6	2737	83.9	651	9	US-10-108-605-75
7	2039.5	62.5	654	10	US-09-919-172-54
8	2010	61.6	653	10	US-09-759-010-2
9	1433.5	43.9	660	10	US-09-841-132-446
10	1430.5	43.8	637	10	US-09-815-242-12058
11	1409	43.2	637	10	US-09-759-010-1
12	1409	43.2	638	10	US-09-815-242-10015
13	1404	43.0	638	10	US-09-815-242-13713
14	1399	42.9	620	10	US-09-815-242-11472
15	1389.5	42.6	610	10	US-09-815-242-5559
16	1389.5	42.6	618	10	US-09-815-242-12567
17	1389.5	42.6	618	10	US-09-815-242-12970
18	1388	42.5	635	10	US-09-815-242-11209
19	1373.5	42.1	609	10	US-09-815-242-10740

20	1373.5	42.1	625	9	US-09-712-363-162	Sequence 162, App
21	1334	40.9	607	10	US-09-815-242-13379	Sequence 13379, A
22	1334	40.9	607	10	US-09-815-242-13682	Sequence 13682, A
23	1067	32.7	420	10	US-09-761-534A-6	Sequence 6, Appl1
24	1040	31.9	209	10	US-09-761-534A-12	Sequence 12, Appl1
25	860	26.4	168	10	US-09-864-761-36258	Sequence 36258, A
26	832.5	25.2	509	10	US-09-731-872-389	Sequence 389, App
27	804.5	24.7	840	10	US-09-922-217-1102	Sequence 1102, Ap
28	790.5	24.2	193	10	US-09-864-761-34864	Sequence 34864, A
29	744.5	22.8	848	10	US-09-825-302-766	Sequence 766, App
30	703.5	21.6	474	10	US-09-864-761-34320	Sequence 34320, A
31	698	21.4	530	9	US-10-108-605-171	Sequence 171, App
32	593	18.2	572	10	US-09-801-368-246	Sequence 246, App
33	584	17.9	137	10	US-09-925-301-1519	Sequence 1519, Ap
34	467.5	14.3	210	10	US-09-761-534A-8	Sequence 8, Appl1
35	417.5	12.8	174	9	US-09-971-536-72	Sequence 72, Appl1
36	257.5	7.9	221	10	US-09-864-761-36116	Sequence 36116, A
37	254	7.8	183	10	US-09-941-132-301	Sequence 301, App
38	248.5	7.6	136	9	US-09-991-496-49	Sequence 49, Appl1
39	248.5	7.6	136	10	US-09-874-923-49	Sequence 49, Appl1
40	236.5	7.2	76	10	US-09-864-761-42162	Sequence 42162, A
41	231	7.1	52	10	US-09-864-761-35578	Sequence 35578, A
42	197	6.0	54	10	US-09-864-761-42619	Sequence 42619, A
43	140.5	4.3	6281	10	US-09-815-242-12996	Sequence 12996, A
44	135	4.1	930	10	US-09-815-242-10779	Sequence 10779, A
45	131.5	4.0	2434	10	US-09-815-242-5835	Sequence 5835, Ap

ALIGNMENTS

RESULT 1									
US-09-759-010-3									
Sequence 3, Application US/09759010									
Patent No. US20010034042A1									
GENERAL INFORMATION:									
APPLICANT: Srivastava, Pramod K.									
TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK									
FILE REFERENCE: 8449-135									
CURRENT APPLICATION NUMBER: US/09/759, 010									
CURRENT FILING DATE: 2001-01-12									
NUMBER OF SEQ ID NOS: 11									
SOFTWARE: PatentIn Ver. 2.1									
SEQ ID NO 3									
LENGTH: 641									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-759-010-3									
Query Match									
Best Local Similarity 100.0%; Pred. No. 3.2e-224;									
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MAKAAAGIDLGTTSCVGVROHGKVEIIANDOGKRTTSPVAFPTDTELTGDAKNQYA	60						
DB	1	MAKAAAGIDLGTTSCVGVROHGKVEIIANDOGKRTTSPVAFPTDTELTGDAKNQYA	60						
QY	61	LNPNQTVFADAKRLTGKRGDPVQSDMKHWPQVINDGDKPKVQSYKGETKAFPEEIS	120						
DB	61	LNPNQTVFADAKRLTGKRGDPVQSDMKHWPQVINDGDKPKVQSYKGETKAFPEEIS	120						
QY	121	SMVLTQKMEIAEAYLGYPVTAATITVPATFNDGQATKQACVATGVLWLRINPTAA	180						
DB	121	SMVLTQKMEIAEAYLGYPVTAATITVPATFNDGQATKQACVATGVLWLRINPTAA	180						
QY	181	IAYGDRGKGRNVLIDLDGGCTFDVSLITDDGIFPKVATAGTHLGGEDFDRKLVNH	240						
DB	181	IAYGDRGKGRNVLIDLDGGCTFDVSLITDDGIFPKVATAGTHLGGEDFDRKLVNH	240						
QY	241	IAYGDRGKGRNVLIDLDGGCTFDVSLITDDGIFPKVATAGTHLGGEDFDRKLVNH	240						
DB	241	IAYGDRGKGRNVLIDLDGGCTFDVSLITDDGIFPKVATAGTHLGGEDFDRKLVNH	240						
QY	300	FVEEERKRRKKKDISONKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFYSITRA	300						
DB	300	FVEEERKRRKKKDISONKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFYSITRA	300						

Qy	301	REFECSOLFSTSTLEPEVBEKALRAOKLDKAQOIHDIYLVGSGSTRIPKYOKLLQDFPNRGDLN	360
Db	301	REFECSOLFSTSTLEPEVBEKALRAOKLDKAQOIHDIYLVGSGSTRIPKYOKLLQDFPNRGDLN	360
Qy	361	KSINDEEVAVGAIVOAAIIMGDKSENVODILLIDVAPLSIGLETAGVMTALIKRSTI	420
Db	361	KSINDEEVAVGAIVOAAIIMGDKSENVODILLIDVAPLSIGLETAGVMTALIKRSTI	420
Qy	421	PTKQTOJFTTYSNDQPGVLIQVYEGEBERAMTKDNLLGREFELSGIIPAPRGVPOIEVTFDI	480
Db	421	PTKQTOJFTTYSNDQPGVLIQVYEGEBERAMTKDNLLGREFELSGIIPAPRGVPOIEVTFDI	480
Qy	481	DANGILNVTATDKSTGKRANKITTNDKGRLSKEEIERMVOAEKYEKKADEEVQBERYSAXN	540
Db	481	DANGILNVTATDKSTGKRANKITTNDKGRLSKEEIERMVOAEKYEKKADEEVQBERYSAXN	540
Qy	541	ALESIAFMMKSAVEDEGLKGRISADKKRYLDKQOEYISMLDANTLAEKDEFHKKRELE	600
Db	541	ALESIAFMMKSAVEDEGLKGRISADKKRYLDKQOEYISMLDANTLAEKDEFHKKRELE	600
Qy	601	QVCNPIISGLYQAGGPGGSGFGAOGKRGSGSGSPTEEVD 641	
Db	601	QVCNPIISGLYQAGGPGGSGFGAOGKRGSGSGSPTEEVD 641	

```

1      RESULT 2
2      US-09-761-534A-10
3      ; Sequence 10, Application US/09761534A
4      ; Patent No. US20020146426A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Huang, Qian
7      ; APPLICANT: Richmond, Joan F.L.
8      ; APPLICANT: Cho, Bryan K.
9      ; APPLICANT: Palliser, Deborah
10     ; APPLICANT: Chen, Jianshu
11     ; APPLICANT: Eisen, Herman N.
12     ; APPLICANT: Young, Richard A.
13     ; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
14     ; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
15     ; TITLE OF INVENTION: CD4+T Cell-Independent
16     ; FILE REFERENCE: 0399.2006-003
17     ; CURRENT APPLICATION NUMBER: US/09/761,534A
18     ; CURRENT FILING DATE: 2001-01-16
19     ; PRIOR APPLICATION NUMBER: PCT/US00/32831
20     ; PRIOR FILING DATE: 2000-12-01
21     ; PRIOR APPLICATION NUMBER: US 60/176,143
22     ; PRIOR FILING DATE: 2000-01-14
23     ; NUMBER OF SEQ ID NOS: 25
24     ; SOFTWARE: FastSeq for Windows Version 4.0
25     ; SEQ ID NO 10
26     ; LENGTH: 642
27     ; TYPE: PRT
28     ; ORGANISM: Unknown
29     ; FEATURE:
30     ; OTHER INFORMATION: Murline hsp70
31     ; US-09-761-534A-10

```

	Query Match	95.8%	Score 3125.5	DB 10;	Length 642;
	Best Local Similarity	95.2%	Pred No. 1.9e-214;		
	Matches 611; Conservative	20;	Mismatches 10;	Indels 1;	Gaps 1;
QY	1	MAKAAAGIDLTCTTSCVGFQHGKVEIIANOGKRRTTPSYAFDTERTLIGDAKNQYA	60		
Dd	1	MAKNNAIGDLCITTSYCVGFQHGKEVEIIANOGKRRTTSPYAFDTERTLIGDAKNQYA	60		
QY	61	LNPQTVDPAKRLIGRKRGDPVVOGDMKHMPQVINDGDGPKPVQVSYSKGETAFFPEETS	120		
Dd	61	LNPQTVEDAKRLIGRKFEGDAYVOGDMKHMPQVVNDGDGPKPVQVNYKGESSFPPEETS	120		
QY	121	SMVLTKMEIEAAYIGYPPTNAVITYPAFENSOQAATRDACVLAGNLRLIINEPTAA	180		
Dd	121	SMVLTKMEIEAAYIGHPTNAVITYPAFENSOQAATRDACVLAGNLRLIINEPTAA	180		

QY	181	IAGLDIRGKERNVLLFDDGGCFEDYSILITIDGIEFVATAGDHPHGGEDDNRLVNH	240
Db	181	IAYGDIRGKERNVLLFDDGGCFEDYSILITIDGIEFVATAGDHPHGGEDDNRLVSH	240
QY	241	FVEEFKRKHKKDDISQNKRAVRLTACEERAKRTLSSSTQASLEIDS:FFEDIDEYTSITRA	300
Db	241	FVEEFKRKHKKDDISQNKRAVRLTACEERAKRTLSSSTQASLEIDS:FEGIDEYTSITRA	300
QY	301	RFEEICSLFESTLEPEPEKALROAKLDKAQIHDLVLVGGSTRIPKQKLLQDPFNROLN	360
Db	301	RFEEICSLFESTLEPEPEKALROAKMDKAQIHDLVLVGGSTRIPKQKLLQDPFNRODIN	360
QY	361	KSINDEAVAGAAVOAAILMGDSENVODLLDLVAPILSLGETAGVATALIKRNSTI	420
Db	361	KSINDEAVAGAAVOAAILMGDSENVODLLDLVAPILSLGETAGVATALIKRNSTI	420
QY	421	PTKQTFPTVYSDNOPGVLIQVYEGEBRMTKDNLLGRFELSGTIPPAKPGVPOIEVTFDI	480
Db	421	PTKQTFPTVYSDNOPGVLIQVYEGEBRMTDNMLLGRFELSGTIPPAKPGVPOIEVTFDI	480
QY	481	DANGILNLTARDKSTGKANKTTITNDGRLSKEIEHMOEAEKYKAEDEVOEERVSANK	540
Db	481	DANGILNLTARDKSTGKANKTTITNDGRLSKEIEHMOEAEKYKAEDEVOEERVAANK	540
QY	541	ALESYAFAFMKSAVEDEGLKGRKISEADKKVLYDKQOEVIYSLMDANTYLAENKDEFHKKRELE	600
Db	541	ALESYAFAFMKSAVEDEGLKGRKLSPADKKVLYDKQOEVIYSLMDSNTLADKREEFVHKKRELE	600
QY	601	QVCNPITISGLYQAGAGRGPGCFAGQG-PRKSGSGGCPITIEVD	641
Db	601	RVCSPITISGLYQAGAGRGPGCFAGQAPPKGASGSGCPITIEVD	642

```

RESULT 3
US-09-870-759-43
; Sequence 43, Application US/09870759
; Patent No. US2002017751A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 646
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-870-759-43

```

[illegible]



OY	246	KRKHKKIDISÖNKRAVRILRTACEPAKRTLSSSTOASLEIDSLEBGDIFYTSTRARPEEL	303
Db	270	RKHOKDKISGNKRRLRLRTACEPAKRTXSSTOTATLEIDSLEBGDVFTYSITRARFEEL	329
OY	306	CSDLEFRSTLEVEPEALNRDAKDKNQHDIVLVGSGSTPIPVOKILODFENGRLOINSINP	365
Db	330	CSDLEFRSTLEVEPEALNRDAKDKNQHIDVVLVGSGSTPIPVOKILODFENGKEIAMSIN	389
OY	366	DEAVALGAAYOAAILMGDSSENOVDLLBLADPALSIGLEFAGGMPTALLIRNSTIPTKOT	425
Db	390	DEAVALGAAYOAAYLMGDKCKEYODLLLDVAPLSJGLEFAGGMWTLIJRNAPTIPTKQ	449
OY	426	QIFTTYSDNOCVLIÖYVEGERAKTONNLIGRELSGITRAPRGVPQIEVTDDANGI	485
Db	450	QIFTTYSDNOCGVFIÖYVEGERAKTKNNNLIGRELSGITRAPRGVPQIEVTDDANGI	509
OY	486	LNTVTDKSTCKANKITTNTNGKLSKEETBERMVOAEKKAKEDVEORREVSVSKNLESY	545
Db	510	LSVATDTSSTCKANKITTNTNGKRLSKEEVERMYHEAOYKADEADORDVAUKNSUEAH	569
OY	546	AFFNMKSAAVEDGLKGKISEADKKRVLLDCQEVLSIMDLANTLAEKDEFERHKKLEJOVCNP	605
Db	570	VFHVKGSIQEBESLRDKIPEEDRRKMÖQKCRVYLAWMLHNQLAKEEVEHQRKRELJOICRH	629
OY	606	IISGLYGAGRGPGRGAGCPKKGSGSGPIIEYD	641
Db	630	IFSRLYGGRGVGGSSCGTQARÖDPSTGPRIIEYD	665

```

RESULT 6
US-10-108-605-75
: Sequence 75, Application US/10108605
: Patent No. US20020160934A1
: GENERAL INFORMATION:
: APPLICANT: Brocdus, Julie
: APPLICANT: Stam, Lynn
: APPLICANT: Bachmann, Jane
: APPLICANT: Kamdar, Kim
: TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
: TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
: FILE REFERENCE: 31133B
: CURRENT APPLICATION NUMBER: US/10/108,605
: CURRENT FILING DATE: 2002-03-27
: PRIOR APPLICATION NUMBER: US 09/761,142
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/176,418
: PRIOR FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 361
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 75
: LENGTH: 651
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
US-10-108-605-75

```

Query Match	83.9%;	Score 2737;	DB 9;	Length 651;
Best Local Similarity	81.3%;	Pred. No. 7.5e-187;		
Matches 529;	Conservative 55;	Mismatches 57;	Indels 10;	Gaps 2;

```

QY 1 MAAAAIGIDIGTTCYSCVGVQHQKVELIANDGCRKTPSYVAFDTJERLIGAAKNQVA 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MSKPAWVIDIGTTCYSCVGVQHQKVELIANDGCRKTPSYVAFDTJERLIGAAKNQVA 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 LNPQNTVDAKRLIGRKGDPVVOQSDKMHMFQVYIINGDGPVKQVYSKGTAKAFPEETS 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 MNPQTFIDARLLIGRKFDDAAVQSDKMHMFEEVYSADGPKTEIVYIKDEKTFPEETS 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 SMVLTKMKEIEALVIGYPVNAVTTPAYFENDSORATKQAGIYAGLNVLRINEPTAAA 180
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SMVLTKMKEIEALVIGKTYTNAVTTPAYFRDSSORATKQAGIYAGLNVLRINEPTAAA 180
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 IAVGLDRTGKGERNVLIIFDLGGGTEDVSIILTDIGIEVATAGDTHLGGEDDNRNLVNH 240

```

```

Db      101  IAYGDKKAVGERNVLFFJDLGGFFDVLSIDGJFEVSTAGDTHLGGEDPDNRVLTH 240
QY      241  FVEEFKRKKHKKDISONKRAVRLTJACERAKRTLSSTQASLSDLSLFEJIDFYSITRA 300
Db      241  FVQEKRRKKHKKDLTTNKRRLRLPTACEBRAKRTLSSSTQASIELDSLFEJIDFYSITRA 300
QY      301  RFEELSDLFIRSTLEPEVEKALRDADLKQAQIHDVLVVGSGSTRIPKVKLLDQFNGRDUN 360
Db      301  RFEELNADLFFRSTMDPYEAKALRDADLKSVIHDVLVVGSGSTRIPKVRLLDQFNGKELN 360
QY      361  KSIINDEAVAVGAOVAAILMGDKSENVODLLLDVAPLSLGLFETAGVWTFALIKRSTI 420
Db      361  KSIINDEAVAVGAOVAAILHGDGSOEYODILLIDVTPSLGIETAGVWVSALIKRNTYI 420
QY      421  PTKQOITTTYSNDQPGVLIOVYEGEBAMTKDNMLGRFELSGIPRAPRCVPOIEVTFPI 480
Db      421  PTKQOITTTYSNDQPGVLIOVYEGEBAMTKDNMLGRFELSGIPRAPRCVPOIEVTFPI 480
QY      481  DANGILANTATDKSTGKANKITITINDGRGLSKEBIEBWMQEAERYKAEDQVGERVSAN 540
Db      481  DANGILANTALERSTENKENTITITINDGRGLSKEDIEBWMVAEAKRYREDEDKQKETTIA 540
QY      541  ALESYAFNMKSAVDEGLKGRKISEADKKVYLDKQCEVYISWLDANTLAEKDEFBHKRKE 600
Db      541  GLESYCFNMKATLDBEDNLKTKTISDSRDTTILDKCNFTIKMLDANQJADKREYBHQKE 600
QY      601  QVCNPTISGLYQGA-----GGPG--PGGFAQGGKGGSGSGSPITTEVD 641
Db      601  GVCNPTIIRKLVQAGFPFGCMGPGGMPGAGGAAGGAGGAGGAPITTEVD 651

```

```

RESULT 7
US-09-919-172-54
: Sequence 54, Application US/09919172
: Patent No. US20020119463A1
: GENERAL INFORMATION:
: APPLICANT: Paris, Mary
: APPLICANT: Turner, Christopher M.
: TITLE OF INVENTION: PROSTATE CANCER MARKERS
: FILE REFERENCE: PA-0036 US
: CURRENT APPLICATION NUMBER: US/09/919,172
: CURRENT FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/222,469
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 102
: SOFTWARE: PERL Program
: SEQ ID NO 54
: LENGTH: 654
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID NO. US20020119463A1 2993696CD1
US-09-919-172-54

```

Query Match	62.5%;	Score 2039.5;	DB 10;	Length 654;
Best Local Similarity	64.4%;	Pred. No. 2.6e-137;		
Matches 398;	Conservative 105;	Mismatches 108;	Indels 7;	Gaps 6;

```

0Y 7 IGIDGTTYSCVGFQHGKXVILINDGGRNRTSPSYAF--DTERLIGDAKKNOVALNPON 65
Db 31 VGIDGTTYSCVGFQHGKNGREILINDGGRNRTSPSYAFTEGREGRLIGDAKKNOULTNSPI 90
0Y 66 TYPFAKRLRIGKRPDDPVYQSMKHMPEOVINDGGRKPVQVSY--KGTEKAPYPEISMTVL 124
Db 91 TYPFAKRLRIGKTMWDPVSQDDIKFLPERVYEKKTPRIQVYDGGGQKTFAPPEISAMVL 150
0Y 125 TKRKEIAEAYGYEPTNAVALTPAYFNDSSROAKTDGAYTAGLNLVRLINEPAAALAAAG 184
Db 151 TKRKEIAEAYLGKRYTAHVYVPEFMDAQROATKQAGTAGLNLVRLINEPAAALAAAG 210
0Y 185 LDRTGKGERNVLFDLGGGTFDVSILVINDGIEFEKATYAGDTHLGGEDPENRLVNHFEVE 244

```

```
Db 211 LDKR-EGEKNILVFDLGGGTFVSLTITDNGVFEVAVATNGDTHLGGEDFDQVAMEHFIXL 269
Qy 245 FKRHKXDISONKRAVRLRTRACERAKRTLSSTQASLEIDSLEEGIDFYSTRARPEE 304
Db 270 YKKTGKDVKRDNRNRAVOKLRREVEKAK-ALSSQHQARIIESFYEGEDFSETLRAKPEE 329
Qy 305 LPSDLFSTLEPVEKALRDADLKAQIHDVLVGGSTRIPKVOKLDOFFNGRDLNKSIN 364
Db 330 LNMFLFSTKMPVOQVLESDLSLKSDDIELVVGSGSTRIPKIQOLVKEFFNGKERSGIN 389
Qy 365 PDEAVAGAAYQAAIILMGDKSENVODLLLDVAPLSLGLTETAGVMTALIKRNSTIPTKQ 424
Db 390 PDEAVAGAAYQAGVLSGD--QDTGDLVLHVCPLTGLIEVGGVMTKLIRNMTVPYTKK 447
Qy 425 TQITFTTSDNQPVLIOYEGEBRATKDNNILGRFELSGIPAPRGVQIETVEDIDANG 484
Db 448 SQIFSTASDNQPTVTIKYEGEBRPLTKDNHLLGTFDLGIPAPRGVQIETVEIDVNG 507
Qy 485 ILNATATDKSTGKANKITITTDKGRLSKEELIERVQAEKAKADEVOERESVAKNALES 544
Db 508 ILRVTAEDEKGTGNKKNKITITDQNRLLPEELERVNDAKEAEEDKILKEHIDTRNLEES 567
Qy 545 YAFNKSASVED-EGIKGKISEADKKVLDKCOEYISWIDANTLAEKDEFEHRRKLEQVC 603
Db 568 YAYSILKNOIGDKELGKLSSEDEKTEMKAVEKEIEMLESHODADIEDFKAKKKELEIY 627
Qy 604 NPITISGLYQAGGPGPG 621
Db 628 QPITISKLY-GSAGPPPTG 644
```

```
RESULT 8
US-09-759-010-2
; Sequence 2, Application US/09759010
; Patent No. US20010034042A1
; GENERAL INFORMATION:
; APPLICANT: Silvastava, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
; FILE REFERENCE: 8449-135
; CURRENT APPLICATION NUMBER: US/09/759,010
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-010-2
```

```
Query Match 61.6%; Score 2010; DB 10; Length 653;
Best Local Similarity 63.9%; Pred. No. 3,2e-135;
Matches 395; Conservative 104; Mismatches 111; Indels 8; Gaps 7;

Qy 7 IGIDGTTTCVGVQFHGKVELIANDQGNRTTPSYAFTRDERLIGDAKNOVALNPONT 65
Db 31 VGIDGTTTCVGVQFKNRVELIANDQGNRTTPSYAFTRPEGERLIGDAKNOQLTSPEN 90
Qy 66 TVPDAKRLIGKRFQDPVVOQDMKHPFOYINDGDKPKVOVAV-KGETAFYPERISAVL 124
Db 91 TVPDAKRLIGKRWDPVSQODIKLFPKVEKRTKPYIOVDIGGQOTFTPAPEISAVL 150
Qy 125 TKMEIAPAYLGYPTNAVITVPAYFNDQSQATKQAGVAGLVNLRTINEPTAAIAYG 184
Db 151 TKMEIAPAYLGYPTNAVITVPAYFNDQSQATKQAGVAGLVNLRTINEPTAAIAYG 210
Qy 185 LDRFGKGRNVLLFDLGGGTFVDSILTDGIEFKAKAGATHGCEGPNRNLVNHFEPE 244
Db 211 LDKR-EGEKNILVFDLGGGTFVDSILTDGIEFKAVATNGDTHLGGEDFDQVMEHFIXL 269
Qy 245 FKRHKXDISONKRAVRLRTRACERAKRTLSSTQASLEIDSLEEGIDFYSTRARPEE 304
```

```
Db 270 YKKTGKDVKRDNRNRAVOKLRREVEKAK-ALSSQHQARIIESFYEGEDFSETLRAKPEE 328
Qy 305 LPSDLFSTLEPVEKALRDADLKAQIHDVLVGGSTRIPKVOKLDOFFNGRDLNKSIN 364
Db 329 LNMFLFSTKMPVOQVLESDLSLKSDDIELVVGSGSTRIPKIQOLVKEFFNGKERSGIN 388
Qy 365 PDEAVAGAAYQAAIILMGDKSENVODLLLDVAPLSLGLTETAGVMTALIKRNSTIPTKQ 424
Db 389 PDEAVAGAAYQAGVLSGD--QDTGDLVLHVCPLTGLIEVGGVMTKLIRNMTVPYTKN 446
Qy 425 TQITFTTSDNQPVLIOYEGEBRATKDNNILGRFELSGIPAPRGVQIETVEDIDANG 484
Db 447 SQIFSTASDNQPTVTIKYEGEBRPLTKDNHLLGTFDLGIPAPRGVQIETVEIDVNG 506
Qy 485 ILNATATDKSTGKANKITITTDKGRLSKEELIERVQAEKAKADEVOERESVAKNALES 544
Db 507 ILRVTAEDEKGTGNKKNKITITDQNRLLPEELERVNDAKEAEEDKILKEHIDTRNLEES 566
Qy 545 YAFNKSASVED-EGIKGKISEADKKVLDKCOEYISWIDANTLAEKDEFEHRRKLEQVC 603
Db 567 YAYSILKNOIGDKELGKLSSEDEKTEMKAVEKEIEMLESHODADIEDFKAKKKELEIY 626
Qy 604 NPITISGLYQAGGPGPG 621
Db 627 QPITISKLY-GSAGPPPTG 643
```

```
RESULT 9
US-09-841-132-446
; Sequence 446, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 446
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis serovar D
US-09-841-132-446
```

```
Query Match 43.9%; Score 1433.5; DB 10; Length 660;
Best Local Similarity 48.2%; Pred. No. 2.9e-94;
Matches 318; Conservative 113; Mismatches 186; Indels 43; Gaps 16;

Qy 7 IGIDGTTTCVGVQFHGKVELIANDQGNRTTPSYAFTRDERLIGDAKNOVALNPONT 66
Db 11 IGIDGTTTSCVSMVEGGQPKVIASBGRTPSYAFTRKIGGETLVIGPAKQAVTNPEKT 70
Qy 67 VPDAKRLIGKRFQDPVVOQDMKHPFOYINDGDKPKVOVAVKGETAFYPERISAVLTK 126
Db 71 LASTKRFITGRFSE--VESEIKTVPYK---APNSGGAVPDEBOKLTPEETIGAOILMK 125
Qy 127 MKETAEALGYPTNAVITVPAYFNDQSQATKQAGVAGLVNLRTINEPTAAIAYGID 186
Db 126 MKETAEALGETVTAIVTVPAYFNDQSQATKQAGVAGLVNLRTINEPTAAIAYGID 185
Qy 187 RTGKGRNVLLFDLGGGTFVDSILTDGIEFKAVATNGDTHLGGEDFDQVNLNHFVEBK 246
Db 186 K--EGDKKIAYFVDLGGGTFVDSILTDGIEFKAVATNGDTHLGGEDFDQVNLNHFVEBK 243
Qy 247 RKHAKDISONKRAVRLRTRACERAKRTLSSTQASLEIDSLEEGID-----FYSTR 300
Db 244 KQEGIDLSKDNMALQRLDAEKAKTELGG--VSSTEINQPTITIDANGPKHALTLTLTA 301
Qy 301 RPEELCSLDFRSTLEPVEKALRDADLKAQIHDVLVGGSTRIPKVOKLDOFFNGRDLN 360
```

DB 302 QFELHSSLLERTKOPCAQOLKDKLUSASIDIDVLLVGGSRMPVAOVAVKEIF--GKEPN 360  
QY 361 KSNIPDEAVAYGAAYAAIIMGDKSENVODLLLDVAAPLSLGETAGVMTALIKRSTI 420  
DB 361 KGNPDEAVAYGAAYAAIIMGDKSENVODLLLDVAAPLSLGETAGVMTALIKRSTI 416  
QY 421 PTQOTQITFTTYSNOCVGLIQTVEGERAMTKNNLLGREFLSGTPAPRGVPOIEVTEDI 480  
DB 417 PTQOTQITFTTYSNOCVGLIQTVEGERAMTKNNLLGREFLSGTPAPRGVPOIEVTEDI 476  
QY 481 DAAGILNVTADKSTGKANKITTTNDKGRSLKSEIEMVOEAKYAEDEVQERSAKN 540  
DB 477 DAAGILNVTADKSTGKANKITTTNDKGRSLKSEIEMVOEAKYAEDEVQERSAKN 535  
QY 541 ALESYAFNMKSAVEDDEGLKGIKISEADKKRY--LDKQOEYISWLDANTLAEK--DEFE- 593  
DB 536 EADGMIFRAKAVKD--YHKIPALVELYKEIEHIEKRYOAIK-EDASTAIKAASDELST 592  
QY 594 HKRKELE---QVCNPIISGLYQAGGPG-----PGFGAOGPRKGGSGG--PTIEVD 641  
DB 593 HMOKIGEMAOQASAAASANAAGGPNINSEDLKKHSFSTRPPAGGSASTDNIEDAD 652

.. RESULT 10  
US-09-815-242-12058  
; Sequence 12058, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Cair, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12058  
; LENGTH: 637  
; TYPE: PRF  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-12058

Query Match 43.8%; Score 1430.5; DB 10; Length 637;  
Best Local Similarity 49.5%; Pred. No. 4.5e-94;  
Matches 310; Conservative 106; Mismatches 179; Indels 31; Gaps 14;

QY 7 IIGIDGTTTSCVGVFOHKGVEIANDQGNRTTSPSYAFT--DTERLIGDAKNOVALNPON 65  
DB 5 IIGIDGTTTSCVGVFOHKGVEIANDQGNRTTSPSYAFT--DTERLIGDAKNOVALNPON 64  
QY 66 TTFDAKRLIGRRFGDPVVOGDMKHPFOYI--NDGDKPRVVOYSYKGETKAFYPEEISSMY 125

DB 65 TTYAVRLLIGRRFEEENVQKDQMPYSLVK-ADNGDAWEYKQKMA--PQISAEVLR 121  
QY 126 KMEIEAAYGVYTVNAVTVPAYFENDSORQATKADGAVLNLVINEPTAAALAYGL 185  
DB 122 KMKKTADVLGEVTEAVITVPAYFENDSORQATKADGAVLNLVINEPTAAALAYGL 181  
QY 186 DRTGGERNVLLFDLGGGFEDVSIPLTD--DG--IFEVKATAGDTHLGGEDPDNRLVNH 241  
DB 182 DK-AKGDHVIYVLDGGGFEDVSIPLTD--DG--IFEVKATAGDTHLGGEDPDNRLVNH 240  
QY 242 VEEFKRKHKKIDSONKRAVRRLTACEKAKRTLSSTQASLEDSIFEGID----FYTSI 297  
DB 241 VEEFKRKHKKIDSONKRAVRRLTACEKAKRTLSSTQASLEDSIFEGID----FYTSI 300  
QY 298 TRARFEELSDLPSTLEPEKALRAKIDKAOIHLVIVGSGSTRIPKYLQDPFNR 357  
DB 301 SRKLESVLEDVQRTIEFCRTALKAGLDVSIHEVIVGGOTRMPYQKTYAEFF--GK 359  
QY 358 DLNKSINPDEAVAYGAAYAAIIMGDKSENVODLLLDVAAPLSLGETAGVMTALIKR 417  
DB 360 EARKDVNPDEAVAYGAAYAAIIMGDKSENVODLLLDVAAPLSLGETAGVMTALIKR 415  
QY 418 STPTQOTQITFTTYSNOCVGLIQTVEGERAMTKNNLLGREFLSGTPAPRGVPOIEVT 477  
DB 416 STPTQOTQITFTTYSNOCVGLIQTVEGERAMTKNNLLGREFLSGTPAPRGVPOIEVT 475  
QY 478 FDIIDANGILNVTADKSTGKANKITTTNDKGRSLKSEIEMVOEAKYAEDEVQERS 537  
DB 476 FDIIDANGILNVTADKSTGKANKITTTNDKGRSLKSEIEMVOEAKYAEDEVQERS 534  
QY 538 AKNALESYAFNMKSAVEDDEGLKGIKISEADKKRYLDKQOEYISWLDANTLAEK--DEFE 596  
DB 535 ARNOGALVHATRKMITTEAGDK--ATFADKATIER--ALGELAAVAVGDDKAEIEAKM 588  
QY 597 KELEQVCNPIISGLY-----QGAGCP 617  
DB 589 NALSOASTPLAOKMYAEQAQGGEDAP 614

.. RESULT 11  
US-09-759-010-1  
; Sequence 1, Application US/09759010  
; Patent No. US20010034042A1  
; GENERAL INFORMATION:  
; APPLICANT: Sivasava, Pramod K.  
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK  
; FILE REFERENCE: 8449-135  
; CURRENT APPLICATION NUMBER: US/09/759,010  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 637  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-09-759-010-1

Query Match 43.2%; Score 1409; DB 10; Length 637;  
Best Local Similarity 51.0%; Pred. No. 1.5e-92;  
Matches 314; Conservative 91; Mismatches 175; Indels 36; Gaps 14;

QY 7 IIGIDGTTTSCVGVFOHKGVEIANDQGNRTTSPSYAFT--DTERLIGDAKNOVALNPON 65  
DB 4 IIGIDGTTTSCVGVFOHKGVEIANDQGNRTTSPSYAFT--DTERLIGDAKNOVALNPON 63  
QY 66 TTFDAKRLIGRRFGDPVVOGDMKHPFOYI--NDGDKPRVVOYSYKGETKAFYPEEISSMY 123  
DB 64 TTFDAKRLIGRRFGDPVVOGDMKHPFOYI--NDGDKPRVVOYSYKGETKAFYPEEISSMY 118  
QY 124 LTKMEIAEAYIGYPTNAVTVPAYFENDSORQATKADGAVLNLVINEPTAAALAY 183

Db 119 LKKKKTAEDYLGEBVTAEVITVPAYFNDAORATKDGRIAGLEVKRIINEPTAAALAY 178  
QY 184 GLDRTGGERVNLFEFDLGGTFEDVSIITFD--DG--IFEVATAGDTHLGGEDDNRNVN 239  
Db 179 GLDK-GTGNRTIAYVDLGGTFEDISITIEDVDEKTEFVATNGDTHLGGEDDSRLIN 237  
QY 240 HFEVEFRKHKRDISQNKRAVRRLTACERAKRTLSSTOASLEIDSLEGI---DEYT 295  
Db 238 YLVEEFKKDGDIDLRNDPLAMQRLKEAEKAKIELSSAQOTDVNLPYITADATGPKHNI 297  
QY 296 SITRAFEELCSDFRSTLEFEVEKALBDKAKQIHDLVYVGSTRIAPKYOGLLODFN 355  
Db 298 KVTBAKLESLVEDLVNRISIEPLKVALODAGLSVSDIDVILVGGOTRPMVQKVAEEF- 356  
QY 356 GRDLKNSINDEAVAYGAAYOAILMGDKSENODLLLDVAPISLGETAGVYATLAK 415  
Db 357 GKPRKQVNPDEAVAIAGAAVGGVLTGD---VKDVLLDVTPISLGETAGVYATLAK 412  
QY 416 NSTIPTKQTIPTTYSNQGVLIOYVEGERAMTKDNLLGREFELSGIPAPRGVPOIE 475  
Db 413 KNTIPTKHSQVSTAEADNQSAVTIHYLQGERKRAADKKSIGQFNLDGINAPRGMPQIE 472  
QY 476 VTEDIDANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOEAEKYAEDEVORER 535  
Db 473 VTFDIDADGILHVSADKNSGKEOKITIKASSG-LNEDEIQKVRDAEAMAEADRKFEEL 531  
QY 536 VSAKNALAEVAFNMKSAVEDEGLKGISADKKVLDKQGVISMLDANTLAEXDE--- 591  
Db 532 VQTRNQGDLHLSRKYOEAGDK--LPADKTAIE-----SALTALLETALKEGDKAA 582  
QY 592 FEHKKRELEQVNCPII 607  
Db 583 IEAKMQELAOVSOKLM 598

RESULT 12  
US-09-815-242-10015  
; Sequence 10015, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10015  
; LENGTH: 638  
; TYPE: PRT  
; ORGANISM: Escherichia coli

US-09-815-242-10015  
Query Match 43.2%; Score 1409; DB 10; Length 638;  
Best Local Similarity 51.0%; Pred. No. 1,56-92;  
Matches 314; Conservative 91; Mismatches 175; Indels 36; Gaps 14;  
QY 7 IGIDGTTQVGVQHQHKEVLIANDGNRTTPSVAFV-PTERLIGDAPNOVALNPON 65  
Db 5 IGIDGTTNSCVALLDGTTPVLENAESGDRTPSLIATQGETVLVGGPARQAVTNON 64  
QY 66 TVFDKRLIGRKGFPDVVQSDMKHWPQVI--NDGDKFQVQSYKGETKAFYPERISSMV 123  
Db 65 TLPAIKRLIGRQFQDEEVQRDVSIIMFKITAADND---AWVEYKQDMA--PQISAY 119  
QY 124 LTKKKEIENATLGPYNAVITVPAYFNDSORATKDGAVIAGLVRLINEPTAAALAY 183  
Db 120 LKKMKTAEDYLGEBVTAEVITVPAYFNDAORATKDGRIAGLEVKRIINEPTAAALAY 179  
QY 184 GLDRTGGERVNLFEFDLGGTFEDVSIITFD--DG--IFEVATAGDTHLGGEDDNRNVN 239  
Db 180 GLDK-GTGNRTIAYVDLGGTFEDISITIEDVDEKTEFVATNGDTHLGGEDDSRLIN 238  
QY 240 HFEVEFRKHKRDISQNKRAVRRLTACERAKRTLSSTOASLEIDSLEGI---DEYT 295  
Db 239 YLVEEFKKDGDIDLRNDPLAMQRLKEAEKAKIELSSAQOTDVNLPYITADATGPKHNI 298  
QY 296 SITRAFEELCSDFRSTLEFEVEKALBDKAKQIHDLVYVGSTRIAPKYOGLLODFN 355  
Db 298 KVTBAKLESLVEDLVNRISIEPLKVALODAGLSVSDIDVILVGGOTRPMVQKVAEEF- 357  
QY 356 GRDLKNSINDEAVAYGAAYOAILMGDKSENODLLLDVAPISLGETAGVYATLAK 415  
Db 357 GKPRKQVNPDEAVAIAGAAVGGVLTGD---VKDVLLDVTPISLGETAGVYATLAK 412  
QY 416 NSTIPTKQTIPTTYSNQGVLIOYVEGERAMTKDNLLGREFELSGIPAPRGVPOIE 475  
Db 413 KNTIPTKHSQVSTAEADNQSAVTIHYLQGERKRAADKKSIGQFNLDGINAPRGMPQIE 472  
QY 476 VTEDIDANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOEAEKYAEDEVORER 535  
Db 473 VTFDIDADGILHVSADKNSGKEOKITIKASSG-LNEDEIQKVRDAEAMAEADRKFEEL 531  
QY 536 VSAKNALAEVAFNMKSAVEDEGLKGISADKKVLDKQGVISMLDANTLAEXDE--- 591  
Db 532 VQTRNQGDLHLSRKYOEAGDK--LPADKTAIE-----SALTALLETALKEGDKAA 582  
QY 592 FEHKKRELEQVNCPII 607  
Db 584 IEAKMQELAOVSOKLM 599

RESULT 13  
US-09-815-242-13713  
; Sequence 13713, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23

```

; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13713
; LENGTH: 638
; TYPE: PRP
; ORGANISM: Salmonella typhi
; US-09-815-242-13713

Query Match      43.0%; Score 1404; DB 10; Length 638;
Best Local Similarity 50.2%; Pred. No. 3,4e-92;
Matches 307; Conservative 95; Mismatches 183; Indels 26; Gaps 13;

QY 7 IGDIDGTTSCVGFPHGVEIILANDQGRNTPTSYAFT-DTERLIGDAKNOVALNPON 65
   ||||| ||| : : : ||||| : ||| : ||| |||
DB 5 IGDIDGTTSCVALMDGTARVLENAEGDRTPTSIATYQDGETLVGQPKRAQAVTNPON 64
   ||| ||||| ||| : ||| : ||| : ||| : ||| : |||
QY 66 TVFDARLIGRKFGDPVYOSDMKHPFOVINODGKPKVOYSYKGETKAFYPEREISSMVL 125
   ||| ||||| ||| : ||| : ||| : ||| : ||| : |||
DB 65 TLEFAIKRLIGRRQDEVEYQDSIMPKIIG-ADNGDAILDVYQKMA--PPQISAEVLK 121
   ||| ||||| ||| : ||| : ||| : ||| : ||| : |||
QY 126 KKEIIEAVLYGYPVNAVTTPAYFENDSORQATKDAVAGIAGLVNLTINEPTAAIAYGI 185
   ||| ||||| ||| : ||| : ||| : ||| : ||| : |||
DB 122 KMKRTAEDYLGEPYAVITVPAYFENDAQROATKDAIRIAGLEVKRLINPTAAALAYGI 181
   ||| ||||| ||| : ||| : ||| : ||| : ||| : |||
QY 186 DRGKERNVILFDLGGGFEDVSIILTD--DG--IEFKATADDTLGGDEPNRLVNH 241
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| ||| |||
DB 182 DKE-VENRTIAYVDLGGGFDSIIIEIDVDGKTEVLTATNGDTHLGGDFDTPLINYL 240
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| ||| |||
QY 242 VEEFKKHKKDIISONKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGT---DFTYTSI 297
   ||||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 241 VEEFKKDDGIDLNDPLAMORLKEAEKAKIELSSAQODTVNLPTIADATGPKHNNIV 300
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 298 TRAREPCLSDLEFRSTLEPERKALRDAKLIDVAVGSGFRIPKVOYLQDFPNGR 357
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 301 TRAKLESLVEDLVNRSIEPLKVALODAGLSVSDINVIIVGQTRPMVQKVAEEFF-GK 359
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 358 DLNKSINPEAVYGAAYQAAILMGDSKSEVODLLLDVAPLSLGETAGVMTALIKRN 417
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 360 EPRKDVNPDEAVAIAGAAYGVLTGD---VKDVLILDVTPLSLGETMGVMTPLITKN 415
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 418 STIPKQTOFTTYSNODPGVLIQVYEGGERAMTKDNMLLGRFELSGIPAPRGVPOIEV 477
   ||||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 416 TITPTHSQVFAEDNQSASVTIIVHLOGEKRAKSDNKSISLQGFLLDGINAPRPMQIEV 475
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 478 FDIIDANGILNVTATDKSTGKANKITTTNDKRLSKEEIERMVOEAKYAEDEVQERVS 537
   ||||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 476 FDIIDANGILNVTATDKSTGKANKITTTNDKRLSKEEIERMVOEAKYAEDEVQERVS 534
   ||||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 538 AKKALESYAFNMKSAVEDSELKGISEADKKVLDKQCEVYISWLDANTLAE-KDEFEHR 536
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 535 TRQGHLLHSTFRQVEAG--DKLPADKTAI---ESALSALETALGEGDAIAEAKN 588
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 597 KELEQVCNPII 607
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 589 QELAQVSQKLM 599
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||

```

```

; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes In
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11472
; LENGTH: 620
; TYPE: PRP
; ORGANISM: Helicobacter pylori
; US-09-815-242-11472

Query Match      42.9%; Score 1399; DB 10; Length 620;
Best Local Similarity 48.0%; Pred. No. 7,4e-92;
Matches 293; Conservative 115; Mismatches 172; Indels 30; Gaps 11;

QY 7 IGDIDGTTSCVGFPHGVEIILANDQGRNTPTSYAFTD--ERLIGDAKNOVALNPON 65
   ||||| ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 5 IGDIDGTTSAMAVYVGNKAKIELANKEGNTPTSYAFTDKGILYGEAKRAQAVTNPER 64
   ||| ||||| ||| : ||| : ||| : ||| : ||| : |||
QY 66 TVFDARLIGRKFGDPVYOSDMKHPFOVINODGKPKVOYSYKGETKAFYPEREISSMVL 125
   ||| ||||| ||| : ||| : ||| : ||| : ||| : |||
DB 65 TYSIRIRMGIMENEDKAEKAEKRLPYKIVDRNGACAIETIS---GKIYTPQESAKILM 120
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 126 KKEIIEAVLYGYPVNAVTTPAYFENDSORQATKDAVAGIAGLVNLTINEPTAAIAYGI 185
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 121 KLEDEASTYGESVTAIVTVPAYFENDSORKATKEAGTIAGLVNLTINEPTAAIAYGI 180
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 186 DRGKERNVILFDLGGGFEDVSIILTDGIEFKATADDTLGGDEPNRLVNHVEEP 245
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 181 DKE--KSEKIMYVDLGGGFEDVYLETGNVYEVLTGDAFLGDDFPNRYVIDFLAEP 238
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 246 KKKHKKDIISONKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGT-----FTYSTR 299
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 239 KNETGIEIKNDVVALORLKEAENAKKELSSAMET--EINLPFITADATGPKHLYKRLR 296
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 300 ARFEELCSDLFRSTLEPERKALRDAKLIDVAVGSGFRIPKVOYLQDFPNGR 359
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 297 AKRESLTEDLVETRTISKISVIRKDALITNEISEVWVGSGFRIPKVOYRVAEFLN-KEL 355
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 360 NKSINPEAVYGAAYQAAILMGDSKSEVODLLLDVAPLSLGETAGVMTALIKRNT 419
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 356 NKSVPNPDEAVYGAAYQVLTGD---VKDVLILDVTPLSLGETMGVMTPLITKN 411
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 420 IPTKQTOFTTYSNODPGVLIQVYEGGERAMTKDNMLLGRFELSGIPAPRGVPOIEV 479
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 412 IPAKKSQVFAEDNQSASVTIIVHLOGEKRLARNDKSLGKFDLGIAPAPRGVPOIEV 471
   ||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
QY 480 IDANGILNVTATDKSTGKANKITTTNDKRLSKEEIERMVOEAKYAEDEVQERVS 539
   ||||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||
DB 472 IDANGILNVTATDKSTGKANKITTTNDKRLSKEEIERMVOEAKYAEDEVQERVS 530
   ||||| : : : ||||| ||| : ||| ||| ||| ||| ||| |||

```

```

RESULT 14
US-09-815-242-11472
; Sequence 11472, Application us/09815242
; Patent No. us2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert

```



QY 540 NALSFYAFNMKSAVEDGLKGRKISEADKKVLDKCOEYISWLD--ANTLAEKDEFEHR 596  
 Db 531 NHAOSLHMQTKSLDEH--KTNLNMENANET----QNAINMLKOCIKRNDNTKAELEBKT 584  
 QY 597 KELBOVCNPI 606  
 Db 585 KALTOAAOKL 594

RESULT 15  
 ; Sequence 5559, Application US/09815242  
 ; Patent No. US20020061569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Karl L.  
 ; APPLICANT: Zyskind, Judith W.  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John D.  
 ; APPLICANT: Carr, Grant J.  
 ; APPLICANT: Yamamoto, Robert T.  
 ; APPLICANT: Xu, H. Howard  
 ; TITLE OF INVENTION: Identification of Essential Genes in  
 ; FILE REFERENCE: ELITRA.011a  
 ; CURRENT APPLICATION NUMBER: US/09/815,242  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 14110  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5559  
 ; LENGTH: 610  
 ; TYPE: FRT  
 ; ORGANISM: Staphylococcus aureus  
 ; US-09-815-242-5559

Query Match 42.6%; Score 1389.5; DB 10; Length 610;  
 Best Local Similarity 47.3%; Pred. No. 3.4e-91;  
 Matches 302; Conservative 111; Mismatches 179; Indels 47; Gaps 12;  
 QY 7 IGIDIGTYSCGVFQDHKVEIIANDQGNRTTPSYAFTDETRLIGDAKNOVALNPONT 66  
 Db 5 IGIDIGTNSCTVLEGEDEPKYQNPESRTTPSYAFAKNGEYQGEVAKRAIITNP-NT 63  
 QY 67 VFDARLLIGRKFEDPVVSDMKHMPFOYINDGDKPRVOYSYKGETKAFYPEEISSMVLTK 126  
 Db 64 VOSIRHHMGTDY-----KVDI---EGKSYTPPEISAMIIQN 96  
 QY 127 MKETAEALGYVTNAVITPAYENDSQRATKDGAVTAGLAVLRIINEPTAAATAYGLD 186  
 Db 97 LKNTAESYLVGEVDAVITVPAYFENDAEKQATKDGAGTAGLEVERIINEPTAAALAYGLD 156  
 QY 187 RTGGERNVLLIFDLGGGTEDVSIITIDGIFEFKATAGDTHLGGEFDNRILVNHFFVEERK 246  
 Db 157 KTDKBER-VLYVDLGGGTEDVSIILELGDGVFEVFLSTAGDNKLGSDDEFOYIIDIYVAERK 215  
 QY 247 RKHKKDISQNKRAVRLTACERAKRLS--SSQASLEFIDSLFEG--IDFYTSITRRARF 302  
 Db 216 KENGVDLSQDKMALQRLKDAERAKKRLSGVSGQTQISLPFISAGENGPLHLEVNLTRSKF 275

QY 303 EELCSDFRSTLEPEVEKALRDALKQAQIHDVLVGGSTRIPKYOKLLODFPNRDLNKS 362  
 Db 276 EELSDSLRRTRMEPTROMKQAGLINSIDDEVILVGGSTRIPAYQEAARKET-GKEPRKG 334  
 QY 363 INPDEAVYGAAYQAAIIMGDKSENVODLLIDVAPLSLGLETAGGVWTFALIKRSTIPT 422  
 Db 335 VNPDEVAMGAAYIOGCVITGD----VKDVLVDVYPLSLGIEILGGRMNTLIERWTIPT 390  
 QY 423 KOTOFETTSYDNQGVLLQYVEGERAMTKDNNLGRFELSGIPPARGVPOIETVFDIDA 482  
 Db 391 SKSQYSTAADNQPVDVHVLQGERPMADNKTGLRFQTDIPPAERKGPQIETVFDIDK 450  
 QY 483 NGILNVATDTSKGRANKITTTNDKGRLSKEIEHMYOEAERYKAEDEVOREVYSAKNAL 542  
 Db 451 NGIYVNTAKDLGTNKQRIITIOSSSS-LSDEIDRMVADAEVNAEADKKRREYDLRNEA 509  
 QY 543 ESYAFNMKSAVEDGLKGRKISEADKKVLDKCOEYISWLDANTLAEKDEFEHRKRELQY 602  
 Db 510 DSIYFQVEKTYLTDLG--ENIGEEDKSAEERKKDALKTALLEGODI--EDIKRKELEKRV 564  
 QY 603 CNPLISGLYOGAGGPGGPGFQAGPFGGSGSGSPTEIYVD 641  
 Db 565 IOELSAKYEQAAQOQO---QAGANAGQNDSTVEDAE 600

Search completed: December 4, 2002, 16:44:35  
 Job time : 14 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:41:27 : Search time 16 Seconds  
(without alignments)  
1178.736 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 3263  
Sequence: 1 MAKAAAGIDLTGTTSCVGV.....FGAGPKGSGSGPTIEVD 641

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCrUS.COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2859.5	87.6	890	4	US-09-513-783A-174 Sequence 174, App
2	2856.5	87.5	646	1	US-08-441-139-14 Sequence 14, Appl
3	2717	83.3	643	4	US-08-797-358B-3 Sequence 3, Appl
4	2088.5	64.0	655	4	US-09-632-538C-36 Sequence 36, Appl
5	2052.5	62.9	666	1	US-08-441-139-16 Sequence 16, Appl
6	2042.5	62.6	654	1	US-08-441-139-11 Sequence 11, Appl
7	2001.5	61.3	682	1	US-08-441-139-2 Sequence 2, Appl
8	1950.5	59.8	679	1	US-08-441-139-5 Sequence 5, Appl
9	1897	58.1	663	1	US-08-441-139-7 Sequence 7, Appl
10	1476.5	45.2	679	1	US-08-214-583-2 Sequence 2, Appl
11	1438	44.1	641	1	US-08-441-139-4 Sequence 4, Appl
12	1435.5	44.0	649	4	US-09-066-947-5 Sequence 5, Appl
13	1397.5	42.8	616	4	US-09-134-001C-3646 Sequence 3646, Ap
14	1354	41.5	339	2	US-08-928-592-52 Sequence 52, Appl
15	1354	41.5	339	4	US-09-339-972-52 Sequence 52, Appl
16	1335	40.9	607	2	US-08-472-534-5 Sequence 5, Appl
17	1247.5	38.2	600	6	5240706-1 Patent No. 5240706
18	985.5	30.2	315	1	US-08-257-073-7 Sequence 7, Appl
19	818	25.1	941	4	US-09-513-783A-172 Sequence 172, App
20	742	22.7	471	1	US-08-203-905B-2 Sequence 2, Appl
21	728	22.3	472	1	US-08-203-905B-14 Sequence 14, Appl
22	651.5	20.0	999	2	US-08-770-101A-3 Sequence 3, Appl
23	651.5	20.0	999	3	US-09-175-581-3 Sequence 3, Appl
24	623.5	19.2	999	2	US-08-770-101A-1 Sequence 1, Appl
25	625.5	19.2	999	3	US-09-175-581-1 Sequence 1, Appl
26	596.5	18.3	307	4	US-08-858-207A-481 Sequence 481, App
27	560.5	17.2	560	2	US-08-928-692-53 Sequence 53, Appl

28	560.5	17.2	560	4	US-09-339-972-53 Sequence 53, Appl
29	518	15.9	187	6	5196523-13 Patent No. 5196523
30	454	13.9	374	2	US-08-928-692-51 Sequence 51, Appl
31	454	13.9	374	4	US-09-339-972-51 Sequence 51, Appl
32	445	13.6	168	1	US-08-441-139-10 Sequence 10, Appl
33	412	12.6	129	6	5196523-10 Patent No. 5196523
34	326	10.0	599	4	US-09-080-983-9 Sequence 9, Appl
35	316	9.7	80	1	US-08-464-164-4 Sequence 4, Appl
36	316	9.7	80	2	US-08-338-057-4 Sequence 4, Appl
37	316	9.7	80	2	US-08-668-416-4 Sequence 4, Appl
38	286.5	8.8	77	6	5196523-7 Patent No. 5196523
39	286	8.8	549	2	US-08-770-544-6 Sequence 6, Appl
40	274.5	8.4	554	5	PCT-US94-06430-7 Sequence 7, Appl
41	271.5	8.3	554	4	Sequence 7, Appl
42	269	8.2	79	6	5196523-11 Patent No. 5196523
43	254	7.8	183	4	US-09-556-877-301 Sequence 301, App
44	254	7.8	183	4	US-09-620-412C-301 Sequence 301, App
45	248.5	7.6	136	4	US-09-183-861-49 Sequence 49, Appl

ALIGNMENTS

RESULT 1									
US-09-513-783A-174									
Sequence 174, Application US/09513783A									
Patent No. 6416959									
GENERAL INFORMATION:									
APPLICANT: Giuliano, Kenneth A.									
APPLICANT: Kapur, Rayl									
TITLE OF INVENTION: A System for Cell Based Screening									
FILE REFERENCE: 97-022-11									
CURRENT APPLICATION NUMBER: US/09/513,783A									
CURRENT FILING DATE: 2000-02-25									
NUMBER OF SEQ ID NOS: 180									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 174									
LENGTH: 890									
TYPE: PRT									
ORGANISM: Artificial Sequence									
FEATURE:									
OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70									
US-09-513-783A-174									
Query Match									
Best Local Similarity 87.6%; Score 2859.5; DB 4; Length 890;									
Matches 553; Conservative 48; Mismatches 40; Indels 5; Gaps 3;									
QY	1	MAKAAAGIDLTGTTSCVGVFOHGVETIANDQGRTPSYVAFTDRLIGDAKNQYA	60						
DB	245	MSKGPVAVIDIGTYSVGVFOHGVETIANDQGRTPSYVAFTDRLIGDAKNQYA	304						
QY	61	LNPOVTVDARLRIGRKDPVVOVSDMKHWPFOVINDGDKPVQVSYKGETKAFYPERIS	120						
DB	305	MNPFTTVVDARLRIGRRDDAVVOVSDMKHWPFOVINDGDKPVQVSYKGETKAFYPERIS	364						
QY	121	SMVLTKMEIAEAYIGYVTAAVITVPAYFNDOSQATKAGVIAGLVLRINEPTAA	180						
DB	365	SMVLTKMEIAEAYIGYVTAAVITVPAYFNDOSQATKAGVIAGLVLRINEPTAA	424						
QY	181	IAYGDRKGRKERNVLIEDLGGTFDVSILITLDOSEFVKATAGTHLGGDFDRLVNH	240						
DB	425	IAYGDRKGRKERNVLIEDLGGTFDVSILITLDOSEFVKATAGTHLGGDFDRLVNH	484						
QY	241	FVEEKKRHKHDISSQKRAVRRLRTACERAKRTLSSTQASLEIDSLTEGIDFYSTR	300						
DB	485	FIAEKKRHKHDISSQKRAVRRLRTACERAKRTLSSTQASLEIDSLTEGIDFYSTR	544						
QY	301	RPEELCSPLFSTLEPVEKALIDAKLKAQIHDVLVGGSTRIPKRVOKLLODFENGRLN	360						
DB	545	RPEELCSPLFSTLEPVEKALIDAKLKAQIHDVLVGGSTRIPKRVOKLLODFENGRLN	604						
QY	361	KSINDEAVVAQAQAALINGDKSENVQDILLIDVAPLSGLTFAGGVMTALIRNSTI	420						

Db 605 KSNPDEAVAYGAQAAILISGDKSENVDLLLDVTPLSIGIETAGVMTVLKRNMTTI 664  
QY 421 PTKQOIFTTYSNQPGLVLOYEGEGRAMTKDNNLLGFEISGIPAPRGVQIETVPDI 480  
Db 665 PTKQOIFTTYSNQPGLVLOYEGEGRAMTKDNNLLGFEISGIPAPRGVQIETVPDI 724  
QY 481 DANGILNVTATDKSTGKANKITITNDKGRSLKEETIERMVOAEKYEKADEVOERESAKN 540  
Db 725 DANGILNVSANDKSTGKANKITITNDKGRSLKEETIERMVOAEKYEKADEKORDVSSKN 784  
QY 541 ALESYAFNMKSAVEDEGLKGISEADKKVLDKQCEVISMLDANTLAEKDEFEHRRKELE 600  
Db 785 SLESYAFNMKATVEDEKLOGKINDEDKOKILDKCNEIINMLDKNOTAEKEEFHQQEKELE 844  
QY 601 QVCPNPIISGLYOGAGG-PG--PGGF--GAQGPKGSGSGPTIEVD 641  
Db 845 KVCNPIITTKLYOSAGMGPGGFPGGAPPSGASGPTIEVD 890

## RESULT 2

US-08-441-139-14  
; Sequence 14, Application US/08441139  
; Patent No. 5773245  
; GENERAL INFORMATION:  
; APPLICANT: Wilttrup, Dr. Karl D.  
; APPLICANT: Robinson, Anne S.  
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,139  
; FILING DATE: 15-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/089,997  
; FILING DATE: 06-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DIGIGLIO, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 8646  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEO ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 646 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-441-139-14

## Query Match

Best Local Similarity 87.5%; Score 2856.5; DB 1; Length 646;  
Matches 533; Conservative 47; Mismatches 41; Indels 5; Gaps 3;

QY 1 MAKAAAGIDIGITTYSCVGFQHGKVEITANDOGNRTTPSYAFTPEELIGDAKNOVA 60  
Db 1 MSKGRVAGIDIGITTYSCVGFQHGKVEITANDOGNRTTPSYAFTPEELIGDAKNOVA 60

QY 61 INPONTVEDAKRLIGREFGDPVYOSDMKHMPROVINDDGKPKVQYSYKGTAFYPEETS 120  
Db 61 MNPNTNVEFDKRLIGREFDPAVYOSDMKHMPFVNVDAGPKVQYVKQETSFPYEEVS 120  
QY 121 SMVLTKEKEIAEAYLYGAPYNAVITPAVFNDSORATKQAGYTAGLANTLRINEPTAA 180  
Db 121 SMVLTKEKEIAEAYLYGAPYNAVITPAVFNDSORATKQAGYTAGLANTLRINEPTAA 180  
QY 181 IAYGLDRTGGERNVLLFDLGSGTFDVSILTTDDGIFPEVAKATAGDTHLGGEDFMDLVNH 240  
Db 181 IAYGLDKKVAERNVLLFDLGSGTFDVSILTTDDGIFPEVAKATAGDTHLGGEDFMDLVNH 240  
QY 241 FVEEFKRRHKDDISENRAVRRLTACERAKRLSSSTQASLEIDSLEFGIDFYSITTA 300  
Db 241 FIAEFKRRHKDDISENRAVRRLTACERAKRLSSSTQASLEIDSLEFGIDFYSITTA 300  
QY 301 RFEELSDLEFRTSLFEVERALRPAKLDKQIHDVLVVGSGSTRIPKQKLODFPNGRDN 360  
Db 301 RFEELNADLFRCGLDVEKALRPAKLDKQIHDVLVVGSGSTRIPKQKLODFPNGRDN 360  
QY 361 KSNPDEAVAYGAQAAILISGDKSENVDLLLDVAPLSIGIETAGVMTVLKRNMTTI 420  
Db 361 KSNPDEAVAYGAQAAILISGDKSENVDLLLDVAPLSIGIETAGVMTVLKRNMTTI 420  
QY 421 PTKQOIFTTYSNQPGLVLOYEGEGRAMTKDNNLLGFEISGIPAPRGVQIETVPDI 480  
Db 421 PTKQOIFTTYSNQPGLVLOYEGEGRAMTKDNNLLGFEISGIPAPRGVQIETVPDI 480  
QY 481 DANGILNVTATDKSTGKANKITITNDKGRSLKEETIERMVOAEKYEKADEVOERESAKN 540  
Db 481 DANGILNVSANDKSTGKANKITITNDKGRSLKEETIERMVOAEKYEKADEKORDVSSKN 540  
QY 541 ALESYAFNMKSAVEDEGLKGISEADKKVLDKQCEVISMLDANTLAEKDEFEHRRKELE 600  
Db 541 SLESYAFNMKATVEDEKLOGKINDEDKOKILDKCNEIINMLDKNOTAEKEEFHQQEKELE 600  
QY 601 QVCPNPIISGLYOGAGG-PG--PGGF--GAQGPKGSGSGPTIEVD 641  
Db 601 KVCNPIITTKLYOSAGMGPGGFPGGAPPSGASGPTIEVD 646

## RESULT 3

US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-Feb-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 643 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 83.3%; Score 2717; DB 4; Length 643;

Best Local Similarity 81.6%; Pred. No. 1.6e-213;  
Matches 519; Conservative 62; Mismatches 55; Indels 0; Gaps 0;

QY 6 AIGIDGTTTSCVGFQFHGKVEIIANDQGNRTTSPVAFDTDERLIGDAKNOVALNPON 65  
DB 8 AVGIDGTTTSCVGFQFHGKVEIIANDQGNRTTSPVAFDTDERLIGDAKNOVALNPON 67  
QY 66 TVFPAKRLIGKRGDPVYQSDMKHMPFOYINDGDKPKQVQSYKGETKAFYPEEISSMWLT 125  
DB 68 TVFPAKRLIGKRGDPVYQSDMKHMPFOYINDGDKPKQVQSYKGETKAFYPEEISSMWLT 127  
QY 126 KKEETAEAYLGYPYTNNAVITPAYFNDSQROATKAGYIAGINVARIIINEPTAAIAVGL 185  
DB 128 KKEETAEAYLGYPYTNNAVITPAYFNDSQROATKAGYIAGINVARIIINEPTAAIAVGL 187  
QY 186 DRTGGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEDFDNRLVNFVEEF 245  
DB 188 DRTGGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEDFDNRLVNFVEEF 247  
QY 246 KRHKKDISQKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFTYTITRARFEEL 305  
DB 248 KRHKKDISQKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFTYTITRARFEEL 307  
QY 306 CSDFRSTLEPEVEKALRDPAKDPAQIHDLVYVGSTRIPKVOQLIDPFNGDLKKSINP 365  
DB 308 CSDFRSTLEPEVEKALRDPAKDPAQIHDLVYVGSTRIPKVOQLIDPFNGDLKKSINP 367  
QY 366 DEAVAYGAAYQAAIILMGDKSENVODLLLDVAPLSLGLETAGVWTALIKRSTIPKOT 425  
DB 368 DEAVAYGAAYQAAIILMGDKSENVODLLLDVAPLSLGLETAGVWTALIKRSTIPKOT 427  
QY 426 QIFTTYSNQGVLIOYVEGERAMTKDNMLGREFLSGIPAPRGVPOIEVTFIDANGI 485  
DB 428 QIFTTYSNQGVLIOYVEGERAMTKDNMLGREFLSGIPAPRGVPOIEVTFIDANGI 487  
QY 486 LNVATDSTGKANKITTTNDKGRLSKEIEEMVQEAKEYKADEVOBERVSAKANALBSY 545  
DB 488 LNVATDSTGKANKITTTNDKGRLSKEIEEMVQEAKEYKADEVOBERVSAKANALBSY 547  
QY 546 AFNMKSAV-EDGELGKISEADKKVLDKQCEVISMLDANTLAEKDEFHKKRELEQVCNP 605  
DB 548 AFNMKSAV-EDGELGKISEADKKVLDKQCEVISMLDANTLAEKDEFHKKRELEQVCNP 607  
QY 606 IISGLYQAGGPGGFGAQPCKGSGSGPTIEEVD 641  
DB 608 IISGLYQAGGPGGFGAQPCKGSGSGPTIEEVD 643

## RESULT 4

US-09-632-538C-36  
Sequence 36, Application US/09632538C  
Patent No. 6440674  
GENERAL INFORMATION:  
APPLICANT: Mista, Santosh et al.  
TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH  
FILE REFERENCE: 34359  
CURRENT APPLICATION NUMBER: US/09/632,538C  
CURRENT FILING DATE: 2000-08-04  
NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 36  
LENGTH: 655  
TYPE: PRT  
ORGANISM: Pseudotsuga menziesii  
US-09-632-538C-36

Query Match 64.0%; Score 2088.5; DB 4; Length 655;  
Best Local Similarity 65.2%; Pred. No. 3.5e-162;  
Matches 402; Conservative 98; Mismatches 114; Indels 3; Gaps 3;

QY 7 IGIDGTTTSCVGFQFHGKVEIIANDQGNRTTSPVAFDTDERLIGDAKNOVALNPON 66  
DB 29 IGIDGTTTSCVGFQFHGKVEIIANDQGNRTTSPVAFDTDERLIGDAKNOVALNPON 88  
QY 67 VFDKRLIGKRGDPVYQSDMKHMPFOYINDGDKPKQVQSYKGETKAFYPEEISSMWLT 125  
DB 89 VFDKRLIGKRGDPVYQSDMKHMPFOYINDGDKPKQVQSYKGETKAFYPEEISSMWLT 148  
QY 126 KKEETAEAYLGYPYTNNAVITPAYFNDSQROATKAGYIAGINVARIIINEPTAAIAVGL 185  
DB 149 KKEETAEAYLGYPYTNNAVITPAYFNDSQROATKAGYIAGINVARIIINEPTAAIAVGL 208  
QY 186 DRTGGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEDFDNRLVNFVEEF 245  
DB 209 DRTGGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEDFDNRLVNFVEEF 267  
QY 246 KRHKKDISQKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFTYTITRARFEEL 305  
DB 268 KRHKKDISQKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFTYTITRARFEEL 327  
QY 306 CSDFRSTLEPEVEKALRDPAKDPAQIHDLVYVGSTRIPKVOQLIDPFNGDLKKSINP 365  
DB 308 CSDFRSTLEPEVEKALRDPAKDPAQIHDLVYVGSTRIPKVOQLIDPFNGDLKKSINP 387  
QY 366 DEAVAYGAAYQAAIILMGDKSENVODLLLDVAPLSLGLETAGVWTALIKRSTIPKOT 425  
DB 368 DEAVAYGAAYQAAIILMGDKSENVODLLLDVAPLSLGLETAGVWTALIKRSTIPKOT 447  
QY 426 QIFTTYSNQGVLIOYVEGERAMTKDNMLGREFLSGIPAPRGVPOIEVTFIDANGI 485  
DB 428 QIFTTYSNQGVLIOYVEGERAMTKDNMLGREFLSGIPAPRGVPOIEVTFIDANGI 507  
QY 486 LNVATDSTGKANKITTTNDKGRLSKEIEEMVQEAKEYKADEVOBERVSAKANALBSY 545  
DB 508 LNVATDSTGKANKITTTNDKGRLSKEIEEMVQEAKEYKADEVOBERVSAKANALBSY 567  
QY 546 AFNMKSAV-EDGELGKISEADKKVLDKQCEVISMLDANTLAEKDEFHKKRELEQVCNP 604  
DB 548 AFNMKSAV-EDGELGKISEADKKVLDKQCEVISMLDANTLAEKDEFHKKRELEQVCNP 627  
QY 605 PIISGLYQAGGPGG 621  
DB 628 PIISGLYQAGGPGG 644

## RESULT 5

US-08-441-139-16  
Sequence 16, Application US/08441139  
Patent No. 5773245  
GENERAL INFORMATION:  
APPLICANT: Wittup, Dr. Karl D.  
APPLICANT: Robinson, Anne S.  
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: USA  
ZIP: 11530

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-16

```

```

Query Match      62.9%; Score 2052.5; DB 1; Length 666;
Best Local Similarity 64.7%; Pred. No. 3.1e-159;
Matches 400; Conservative 105; Mismatches 106; Indels 7; Gaps 6;

```

```

QY 7 IGIDLGTTCVGVFQHGKVEIILANDOGNRTTPSYAFT-DTERLIGDAKNOVALNPON 65
DB 43 VGIIDLTTCVGVFQHGKVEIILANDOGNRTTPSYAFTPEGRLIGDAKNOULTSPEN 102
QY 66 TVFDARLIGRKRGDPVYSDMKHMPVOVINDGDKPKVOYSY-KGELKAFYPEEISSMYL 124
DB 103 TVFDARLIGRTWNPDSVOODIKFLPKFYVEKKAKPHIQVDVGGGQTKTFAPEISAMVL 162
QY 125 TKKKEIAEALGYPTVNAVITVPAYFNDOSROATKDGAVTAGLNVLRINEPTAAIAYG 184
DB 163 TKKKEIAEALGKVVHNAVTVPAYFNDARQATKDGAGTIAVNMRIINEPTAAIAYG 222
QY 185 LDRTGGERVNLFFDLGGGTFDVSILITIDGIFEVATAGDTHLGGEDPDNRVNHVEE 244
DB 223 LDRR-BGEKNILVFDLGGGTFDVSILITIDGVEEVATNGDTHLGGEDPDQRVMEHPIKL 281
QY 245 FKRHRKDISONKRAVRLTACERAKRTLSSTQASLEIDSLFEGIDFTYSTRARFEE 304
DB 282 YKKTKGDKVAKONRAVOKLREVEKAKRALSQHQARIETIESFEGEDFSETILRAKFE 341
QY 305 LQSDLRSTIEPEYKALRDAKLDKQIHLVLYVGGSTRIPKVKLLODFNGDLKNSIN 364
DB 342 LNNDLRSTIRKPVQXVLESIDLKSDIDEIVLVGGSTRIPKIQVLVEFFNGKEPSGGIN 401
QY 365 PDPAVAYGAOVAAILMGDSENVODLLDVAPLSLGTETAGVMTALIKRSTIPTKO 424
DB 402 PDPAVAYGAOVAIVQAGVLSGD-QDTGDLVYLDDVCPRLTIGITVGVGMTKILPRITVPTKK 459
QY 425 TQIITTVSDNPGVLQVVEGERAMTKDNMLGRFELSGIPPARPGVQIETEVFDIDANG 484
DB 460 SQEFSTASDNQPTVITIKYVGERPLTRKDNHLLGTFDLTGIPPARPGVQIETEVFDIDANG 519
QY 485 ILNVLTIDKSTGKANKITITNDKGRLSKEIEEMVOAEKYYKADDEVQRRYSAKNALES 544
DB 520 ILKVTLEDKGTGKNKRIITINDONRLTPEEIEEMVNDAEKFAEDKKLKERIDARNLELES 579
QY 545 YAFNMKSAVED-EGIKGKISEADKKKVLDDKCOVIVISLMDANTLAEKDEPHKKELEQVC 603
DB 580 YAFSLKNOIGDKELGKLISEDKETIEKAVEKIEIWLESHODADIEDFKSKKELEEVV 639

```

```

QY 604 NPITISGLYOGAGGPGG 621
DB 640 QPIVSKLY-GSAGPPPTG 656

```

```

RESULT 6
US-08-441-139-11
Sequence 11, Application US/08441139
Patent No. 5773245
GENERAL INFORMATION:
APPLICANT: Wittup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-11

```

```

Query Match      62.6%; Score 2042.5; DB 1; Length 654;
Best Local Similarity 64.6%; Pred. No. 2e-158;
Matches 399; Conservative 104; Mismatches 108; Indels 7; Gaps 6;

```

```

QY 7 IGIDLGTTCVGVFQHGKVEIILANDOGNRTTPSYAFT-DTERLIGDAKNOVALNPON 65
DB 31 VGIIDLTTCVGVFQHGKVEIILANDOGNRTTPSYAFTPEGRLIGDAKNOULTSPEN 90
QY 66 TVFDARLIGRKRGDPVYSDMKHMPVOVINDGDKPKVOYSY-KGELKAFYPEEISSMYL 124
DB 91 TVFDARLIGRTWNPDSVOODIKFLPKFYVEKKAKPHIQVDVGGGQTKTFAPEISAMVL 150
QY 125 TKKKEIAEALGYPTVNAVITVPAYFNDOSROATKDGAVTAGLNVLRINEPTAAIAYG 184
DB 151 TKKKEIAEALGKVVHNAVTVPAYFNDARQATKDGAGTIAVNMRIINEPTAAIAYG 210
QY 185 LDRTGGERVNLFFDLGGGTFDVSILITIDGIFEVATAGDTHLGGEDPDNRVNHVEE 244
DB 211 LDRR-BGEKNILVFDLGGGTFDVSILITIDGVEEVATNGDTHLGGEDPDQRVMEHPIKL 269
QY 245 FKRHRKDISONKRAVRLTACERAKRTLSSTQASLEIDSLFEGIDFTYSTRARFEE 304

```

```

Db 270 YKKTKGDKVRKDNRAVOKLRREVEKAKRALSSQHOARIETSEFECEGDFSETLTPAKFEE 329
Qy 305 LCSDFRSTLEPEREKALDADKAQIHDLYVGGSTRIPKYOQLDQFFNCRDLNKSIN 364
Db 330 LMDLFRSTMRKYOKVLEBDSLKSIDELIYVGSTRIPIKQOOLYKFFNKEPSRGIN 389
Qy 365 PDEAAVAAVQAAALIMDKSENVDLLLDVAPLSLGLTETAGVMTLIRKNSIPIPKO 424
Db 390 PDEAAVAAVQAAVGLSD--QDTGDLVLDVLCPLTLGLIETVGGVMTKLIPRNVVPTK 447
Qy 425 TQITFTYSNPGVLLIYQVEGERAMTKDNMLGRRLSGIPAPRGVQIETVPDIDANG 484
Db 448 SOIFSTADNQPVTYIKYEGEGRPLTKDNHLGTFDLGIPAPRGVQIETVFEIDVNG 507
Qy 485 ILNLTATKRSKQKANKITITNDKGRLSKEEIERMVOEAKRYAEDEVORERYSANALE 544
Db 508 ILRYIAEKGKGNKKRKITITNDOMRLTPEEIERMVNDAEKFAEDKRLKERIDTFNELES 567
Qy 545 YAFNKSAAVED-EGLKGRISEADKKVLDKCOEVIISWLDANTLAEKDEFEHKKRELEOV 603
Db 568 YAYSLEKNOIGDEKELGKLSSEDKETMEKAVEKEIEMLESODADIEDKAKKKELEIV 627
Qy 604 NPISGLYQAGAGPGPGC 621
Db 628 QPILSKLY-GSAGPPPTG 644

```

```

RESULT 7
US-08-441-139-2
; Sequence 2, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; NUMBER OF INVENTIONS: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELE: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 682 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-139-2
Query Match 61.3%, Score 2001.5; DB 1; Length 682;

```

```

Best Local Similarity 62.9%; Pred. No. 4,8e-155;
Matches 388; Conservative 102; Mismatches 122; Indels 5; Gaps 4;
Qy 7 IGIDIGTGYSCVGFQPHGKVEILLANDQGNRTTPSYVAFTDERLIGDAKNOVALNPONT 66
Db 53 IGIDIGTGYSCVAVKNGKTEILLANEOGNRTIPSYVAFTDERLIGDAKNOVALNPONT 112
Qy 67 VEDAKRLIGRKFGDPPVSDMKHMPFYVINDGDKKVOYSYKGFETKATYPEEISSMYLT 126
Db 113 IFDILRLIGLKNDRSVOKDILHLPFNVYNDGKPAVEYSVKGKRVPTPEISGMILGK 172
Qy 127 MKEIAEVLGYVTNAVITVPAYFNDOSORATKDGAGVLAGLVNLIINEPTAAATAAGTD 186
Db 173 MKQIADIEDLGTVTYAVTVAPYFNDARQATKQDGTAGLVNLIIVEPTAAATAAGTD 232
Qy 187 RTGGERNVLLPDLGGGFEDVSIITLIDGIEFVKATAGDTHLGEDFDRNLVNHFEERK 246
Db 223 KSDK-EHQIIVYDLGGGFEDVSLIENGVEVQATSGDTHLGEDFPVKIYRLIKAFK 291
Qy 247 RKHKDISONKRAVRLRACERAKRTLSSTQASLEIDSLEFGIDFTTSITRAFEEIC 306
Db 292 KKHGIDVSDNNKALAKLRKAEKAKRALSSQSTRIEIDSFVDGIDLSSETLIRAFEEIN 351
Qy 307 SDFRSTLEPEREKALDADKAQIHDLYVGGSTRIPKYOQLDQFFNCRDLNKSINPD 366
Db 352 LDLEFKTKLPYKVLQDSGLEKKYDDIYVGGSTRIRKYOQLDSYFDGKAKSGINPD 411
Qy 367 EAVVAGAAVQAAALIMDKSENVDLLLDVAPLSLGLTETAGVMTLIRKNSIPIPKOQ 426
Db 412 EAVVAGAAVQAVLGS--EGVEDIYVLDVNLTLGIEFTGVMPPLIRKNTAIPTRKSQ 469
Qy 427 ITFTYSNPGVLLIYQVEGERAMTKDNMLGFEELSGIPAPRGVQIETVPDIDANGTL 486
Db 470 IFTAVDNPQTVMIKYVEBERAMSKDNMLGFEELTGPAPRGVQIETVPDIDANGTL 529
Qy 487 NYTATDKSTGKANKITITNDKGRLSKEEIERMVOEAKRYAEDEVORERYSANALE 546
Db 530 KVSATDKGTGKESITITNDKGRLOEIDRVAVEDEKFAESDASIKAKVESRKULENYA 589
Qy 547 FMNKSAAVEDGLKGRISEADKKVLDKCOEVIISWLDAN-TLAEKDEFEHKKRELEOV 605
Db 590 HSLKNQVNGD-LGKLEEDKETLLDANADVLEWLDNDETAIADFDKPSLSKVAVP 648
Qy 606 ITSGLYQAGAGPGPGC 622
Db 649 ITSGLYQAGAGPGGADY 665
RESULT 8
US-08-441-139-5
; Sequence 5, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; NUMBER OF INVENTIONS: RECOMBINANTLY EXPRESSED PROTEINS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995

```

```

? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/089,997
? FILING DATE: 06-JUL-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: DIGILIO, Frank S.
? REGISTRATION NUMBER: 31,346
? REFERENCE/DOCKET NUMBER: 8646
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 516-742-4343
? TELEFAX: 516-742-4366
? TELEX: 230 901 SASU UR
? INFORMATION FOR SEO ID NO.: 5
? SEQUENCE CHARACTERISTICS:
? LENGTH: 679 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? OS-08-441-139-5

```

Query Match	59.8%;	Score 1950.5;	DB 1;	Length 679;
Best Local Similarity	-60.7%;	Pred. No. 6.9e-151;		
Matches 383;	Conservative 102;	Mismatches 133;	Indels 13;	Gaps 5

OY	1	MAKAA-----	AIIGDLGTTTSCVBOHCQKEIIILANOGNRTPSYVAFLDTLEILG	52
Db	40	VARAABEDHEDYGIYIGDLGTTTSCVAVANKKKEILLANOGNRITPSYVSFTDDERLIG	99	
OY	53	DAAKNOVALNPONTVEFDAKRLIGKRFDPVYVOSDKHMPQVINDGDKPVOVYSYGETK	112	
Db	100	DAAKNOAASNPNKNTIFPIKRLIGLOYNDPQVORIKHLPTVYVANKGKPVYEATVYGEKK	159	
OY	113	AFYEEELSSWLTMKELAEALYGLPYTNNAVITYPAFENDSOQATTDACVYAGLVNLR	172	
Db	160	EFTPEEESGMILGMMKQIAEDYLCKYTHAVVYPAFENDAOBATDACAINGLNLRI	219	
OY	173	INEPTAAAIAGDLRDTCKGERHNVLIFPDAGGTEPVSILTTIDGCFEYKACAGDTIHAGED	232	
Db	220	VNEPTAAAIANGDKT-EDENQIIVYDGGOTPDVSYLSTENGVEFYQATAGDTHAGED	278	
OY	233	FDRNLVNHVEEKKRKKHKDISQNKRAVRRLTACERAKTTLSSSQASLEIDSLEGID	292	
Db	279	FDYKLIYHFAFLFOKRIKHDLYTKNDKMMAKIKREAEKAKRSSQSTRIEISFENGID	338	
OY	293	FYTSITRAREPELSQDLFRSTLBEVEKALBDAKDKQIHDIYVYGSTRIPIPVOKILOD	352	
Db	339	FSETLTRAKFEELMALFKTKLKEVEKVLKDSGLQKEDIDDIYLVYGSTRIPIPVQOLLEK	398	
OY	353	FFNGRDINKSINPDEAAYAGAAYOAAIIMDKSENVODLLILDAVAPLSILETAGVMTA	412	
Db	399	FFNGKAKASKGINPDEAAYAGAAYOAGVLSGE--GCVEDIYLVLDVNALTLGIEFTGGVMP	456	
OY	413	LIRKNSITPTQOTQIFTTYSNQGCVLIQVYEGEGRANTKDNNLGRELSGCTPPAPRGVP	472	
Db	457	LIRKNTALPTKRSQISTFYAVDNQAAVLIQVYEGEGRAYKNNNLGNLFELSDIAAPRGVP	516	
OY	473	QIEVTPDIDANGILNMTATDKSTKAKKNTITNDKGLSKSEETIERMVOAEKKAEDVQ	532	
Db	517	QIEVTFALDANGILTVSATDKDCTKSSITLNDKGLSODDIDRWYEBEKKAADPAK	576	
OY	533	REYVSAKNALESYAFNMKSAVEDEGLKGTISEADKKRYLDDCKQEVISWILDANT-LAEKE	591	
Db	577	KAKSEARNTFENFYHYAKVNSYNGE-LAEIMDEDDKFTVLNDVNSLEMLDENSDDVAEAD	635	
OY	592	FEHNRKLEBOVCNPIISGLVQAGGPPRGCF	622	
Db	636	FEEMASFKESVEPIILAKASQGSTSGEFP	666	

RESULT 9  
US-08-441-139-7  
; Sequence 7, Application US/08441139

```

Patent No. 5773245
GENERAL INFORMATION:
APPLICANT: Wiltup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
City: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-7

```

Query Match	58.1%;	Score 1897;	DB 1;	length 663;
Best Local Similarity	-59.5%;	Pred. NO. 1.6e-146;		
Matches 365;	Conservative 121;	Mismatches 119;	Indels 8;	Gaps 7;

QY	7	IGIDLGTTYSGVGFHQKGVLEIIANDGNRTPTBYAFPTQTEERLISGAARKQVALNPONT	66
Db	38	IGIDLGTTYSCVAAMKNGRVEIILANDGNRTPTBYAFPTQTEERLISGAARKQVALNPONT	97
QY	67	VFDARLRIGRKFSGDPVVQSDMKHMPFOVINDGSRPKVOYSKCYETKAFYPREISSMWLTK	120
Db	98	IFDIKRLRIGRKFDEKTMAKDIKSPFHLYNDKNRPDLVEVNVGKKKFTPEISAMILSK	15
QY	127	MKEIAEAYLGTPVTNAVITTPATFYNDSORQATKQAGYIAGLNVLRINEPEAAAIAAGLD	186
Db	158	MKQFAEAYLGTPVTHSVYTPAYPYNDAORQATKQAGIAGLNVLRINEPEAAAIAAGLD	21
QY	187	RTGGERNVLFIDGGGFEDYSILTIDGJEYVATKAGDFHILGSEDGPNLRVNFVFEK	246
Db	218	KTDPI-EKHIVYIDGGGFEDYSILTIDGJEYVATKAGDFHILGSEDGPNLRVNFVFEK	27
QY	247	RKHKKDISONKRAVRRLTACERAKRPTLSSSTQASLEIDSLFEGIDEYTSITRARFEELC	306
Db	277	RKNNVDTKDLKAMGKTLREVERKANGTSSQSVRIEIESPFNGQDESETLSRAKFEIK	336
QY	307	SDLFRSTLEPERKALRPAKDLKAOIHLVLVYGSGSTRIPKYOQLQDFPNRGDLKSLNPD	366
Db	337	HGSLQEDFEPEYEQVLKXSNLKSLEIDIVLGGSTRIPIKVOELLESFF-CGKASKGAINPD	395
QY	367	EAVYGAAYQAAILMGKSEVQDOLLIDVAPSLSLGLETAGGVNTALIKRSTPIRQTQ	422
Db	396	EAVYGAAYQAAYVLSGE--GGSDIVLIDVAPLPLGLGTTGGVNTKLGKNTPIPIRKSQ	455







|||||  
Db 468 PQIWEVDIDANGIVHSAKAKASGKBQTIKT-QSSGGLSDELEIKKWKADQDAEDEX 526  
QY 532 QREVSASAKNALESTAFNMKSAVEDEBGLKGTSEADKKVLDKCOEVIISWL-DANTLAERD 590  
Db 527 RKKEHVEIKNSSEGLHSHEKSLKDYG--DKYAGADKSNIEISAIKDLRECLNDSN--CSTD 582  
QY 591 EFEKRELEQVCNPIISGLYGAGGPGPGFGAAG-PKGGSSGSPTEEVD 641  
Db 583 TLQOKYDALNMLSMKLGBAATPAANKNDGASADSGSSSSGSDGNPEERYVD 634  
  
RESULT 13  
US-09-134-001C-3646  
; Sequence 3646, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucelte-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3646  
; LENGTH: 616  
; TYPE: PRY  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3646

Query Match 42.8%; Score 1397.5; DB 4; Length 616;  
Best Local Similarity 47.4%; Pred. No. 8.6e-106;  
Matches 303; Conservative 113; Mismatches 174; Indels 49; Gaps 12;  
  
QY 7 IGIDLGTTTSCVGFQHGKVEITANDOGNRTTSPYVAFTEERLIGDAKNOVALNPON 66  
Db 12 IGIDLGTTTSCVGFQHGKVEITANDOGNRTTSPYVAFTEERLIGDAKNOVALNPON 70  
QY 67 VEDAKRLIGKFGDPVVOQSDMKHMPQVINDGKPKVOVSTKGEKAFYPEEISSMYLT 126  
Db 71 VQSKRHKGTDT-----KVDI---EKKSTPELSMILQON 103  
QY 127 MKETAEALYGYPTNAVITPAPYFNDGSRQATKAGVITAGLNVRLINEPAAAIAYGLD 186  
Db 104 LKSTAEALYGYPTNAVITPAPYFNDGSRQATKAGVITAGLNVRLINEPAAAIAYGLD 163  
QY 187 RTGGERNVLIIFDGGGTFFVSIITIDGIFEVAKATAGDTHLGCEPDFNRLVNHFEVEEK 246  
Db 164 KT-ETDQVLIFFDGGGTFFVSIITIDGIFEVAKATAGDTHLGCEPDFNRLVNHFEVEEK 222  
QY 247 RKHKKIDSONKRAYRRLTACEBAKRTLS--STQASLEIDSLFEG--IDYTTSTTRAF 302  
Db 223 KENGVDSQDMALQRLKDAEKAKKDLSGVQTOISLPTISAGENGVLHLSLTRKEF 282  
QY 303 EELCSDFRSTLEPEVKALRDALKDAQIHDVLVVGSGSTRIPKVOYKLDQDFNGHDLKS 362  
Db 283 EELDSLTKTMEPTROLKADAGLSTSEIDVILVCGSTRIPAVQEAANKKEI-CGERPKG 341  
QY 363 INPEBAVAYGAOVAAILMGKSENVODLLDVAAPLSGLFETAGCVTALIKRNSIPT 422  
Db 342 VNPEEVAMGAALQAGVITGD-----VKDQVLIIDVPLSLGIEIMGGRMNTLIERNTTPT 397  
QY 423 KQDIEFTTSSNOGCVLQOYEGEERAMTKDNNLIGREFLSGIPAPRQVPOIEVTFDDA 482  
Db 398 SKSOVYTAANQPAVDIHVLQGERPMAKDKTIGRFOITDIPAPRQVPOIEVTFDDK 457  
QY 483 NGILNVATADKSTGKANKITITNDKRLSKREIERMVOEAKYKADEVOERERYSAKNAL 542  
Db 458 NGIYNVATADKSTGKANKITITNDKRLSKREIERMVOEAKYKADEVOERERYSAKNAL 516

QY 543 ESYAFNMKSAVEDEBGLKGTSEADKKVLDKCOEVIISWL-DANTLAERD 602  
Db 517 DSVLFQVYERTYKTDIG--ENISDEEDKNAEKKRDAKTALBEEEDI--DDIARKEELEKV 571  
QY 603 CNPIISGLYGAGGPGPGFGAAGPGPKGGSSGSPTEEVD 641  
Db 572 IQELSAKYEQAAQQAQOQOGQEGEGSGSDS-----TYEDAD 605

RESULT 14  
US-08-928-692-52  
; Sequence 52, Application US/08928692  
; Patent No. 5958727  
; GENERAL INFORMATION:  
; APPLICANT: Brody, Howard  
; APPLICANT: Yaver, Deborah S.  
; APPLICANT: Lamsa, Michael  
; APPLICANT: Hansen, Kim  
; TITLE OF INVENTION: Methods for Modifying the Production of  
; TITLE OF INVENTION: a Polypeptide  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: No. 59587270 No. 5958727disk of No. 5958727th America, Inc.  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: IBM Compatible  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,692  
; FILING DATE: 12-SEPT-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 4944,200-US  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: linear  
US-08-928-692-52

Query Match 41.5%; Score 1354; DB 2; Length 339;  
Best Local Similarity 76.1%; Pred. No. 1.2e-102;  
Matches 264; Conservative 37; Mismatches 35; Indels 2; Gaps 2;  
  
QY 6 AIGIDLGTTTSCVGFQHGKVEITANDOGNRTTSPYVAFTEERLIGDAKNOVALNPON 65  
Db 4 AIGIDLGTTTSCVGFQHGKVEITANDOGNRTTSPYVAFTEERLIGDAKNOVALNPON 63  
QY 66 TVFDKRLIGKFGDPVVOQSDMKHMPQVINDGKPKVOVSTKGEKAFYPEEISSMYLT 125  
Db 64 TVFDKRLIGKFGDPVVOQSDMKHMPQVINDGKPKVOVSTKGEKAFYPEEISSMYLT 123  
QY 126 MKETAEALYGYPTNAVITPAPYFNDGSRQATKAGVITAGLNVRLINEPAAAIAYGL 185  
Db 124 MKETAEALYGYPTNAVITPAPYFNDGSRQATKAGVITAGLNVRLINEPAAAIAYGL 183  
QY 186 RTGGERNVLIIFDGGGTFFVSIITIDGIFEVAKATAGDTHLGCEPDFNRLVNHFEVEEK 245  
Db 184 DKKK-EEHVLIIFDGGGTFFVSIITIDGIFEVAKATAGDTHLGCEPDFNRLVNHFEVEEK 242



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:40:57 : Search time 37 Seconds  
(without alignments)  
3569.627 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 3263  
Sequence: 1 MAKAAAGIDIGTTCVGV.....FGAAGPKGSGSGPTIEVD 641

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioplasmid:\*  
17: sp\_archaeoplasmid:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3203.5	98.2	640	Q8WNS9	Q8WNS9 canis famill
2	3136	96.1	641	Q9QWJ5	Q9QWJ5 mus musculu
3	3125.5	95.8	642	Q925V6	Q925V6 mus musculu
4	3114	95.4	641	Q63256	Q63256 rattus norv
5	2925	89.6	641	Q75634	Q75634 homo sapien
6	2895	88.6	641	Q96CQ9	Q96CQ9 homo sapien
7	2889	88.5	641	Q88686	Q88686 mus musculu
8	2829	86.7	651	Q8UV14	Q8UV14 ambystoma m
9	2826.5	86.6	646	Q73885	Q73885 gallus galli
10	2820.5	86.4	639	Q73922	Q73922 oreochromis
11	2800.5	85.8	640	Q93240	Q93240 paratichthy
12	2798	85.7	639	Q8UWMS	Q8UWMS xiphophorus
13	2792.5	85.6	650	Q73788	Q73788 paratichthy
14	2792	85.6	655	Q919G5	Q919G5 rivulus mar
15	2789	85.5	658	Q91AC1	Q91AC1 brachydantio
16	2787.5	85.4	644	Q8UWM6	Q8UWM6 oncoerynchu

17	2778	85.1	649	13	P79984	P79984 brachydantio
18	2777	85.1	659	5	Q9XZJ2	Q9XZJ2 crassostrea
19	2763.5	84.7	638	13	Q8UWM0	Q8UWM0 xiphophorus
20	2762.5	84.7	633	11	Q99KD7	Q99KD7 mus musculu
21	2758.5	84.5	658	5	Q27121	Q27121 urechis cau
22	2758	84.5	636	6	Q9YUG3	Q9YUG3 capra hircu
23	2757	84.5	637	13	Q8UWM8	Q8UWM8 xiphophorus
24	2756	84.5	647	13	Q91993	Q91993 xenopus lae
25	2756	84.5	650	5	Q9GPK0	Q9GPK0 heterodera
26	2756	84.5	653	5	Q94805	Q94805 trichoplusi
27	2754.5	84.4	645	5	Q96541	Q96541 setaria dig
28	2753.5	84.4	639	5	Q9NGK9	Q9NGK9 wuchereria
29	2752	84.3	643	13	Q98900	Q98900 figu rubrip
30	2751	84.3	643	6	Q9N1U2	Q9N1U2 saquinavir
31	2747.5	84.2	645	5	Q9N1B7	Q9N1B7 wuchereria
32	2745	84.1	653	5	Q17310	Q17310 ceratilis c
33	2742.5	84.0	644	5	Q9NAX9	Q9NAX9 parastromy
34	2730.5	83.7	640	5	Q93601	Q93601 caenorhabd
35	2728	83.6	651	5	Q8SXQ4	Q8SXQ4 drosophila
36	2721	83.4	656	5	Q61226	Q61226 sycon rapia
37	2715	83.2	643	13	Q8UWU8	Q8UWU8 brachydantio
38	2692	82.5	646	5	Q94614	Q94614 mesocetoid
39	2691	82.5	644	5	Q95V47	Q95V47 artemia san
40	2690.5	82.5	665	5	Q24789	Q24789 echinococcu
41	2665	81.7	646	5	Q01948	Q01948 trichinella
42	2634.5	80.7	663	5	Q24952	Q24952 geodia cydo
43	2619	80.3	645	13	Q91624	Q91624 xenopus lae
44	2580	79.1	566	6	Q95LNG	Q95LNG macaca fasc
45	2567.5	78.7	586	4	Q961S6	Q961S6 homo sapien

## ALIGNMENTS

## RESULT 1

ID Q8WNS9 PRELIMINARY: PRT: 640 AA.  
AC Q8WNS9:  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Heat shock protein 70.  
GN HSP70.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Abe K., Kano R., Hasegawa A.;  
RT "Canine heat shock protein 70 (hsp70) mRNA, complete cds.";  
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB075027; BAB78505.1; -  
DR InterPro: IPR001023; Hsp70.  
DR Pfam: PF00012; HSP70.1  
DR PRINTS: PR000301; HEATSHOCK70.  
DR ProDom: PD000089; HSP70.1.  
DR PROSITE: PS00297; HSP70.1; UNKNOWN.1.  
DR PROSITE: PS00329; HSP70.2; UNKNOWN.1.  
DR PROSITE: PS01036; HSP70.3; UNKNOWN.1.  
SQ SEQUENCE 640 AA: 69935 MW: 40253E91871BF87F CRC64;

Query Match 98.2%; Score 3203.5; DB 6; Length 640;  
Best local similarity 98.3%; Pred. No. 2.1e-174;  
Matches 630; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY	1	MAKAAAGIDIGTTCVGVFQHGKVEIIANDGNGRTTSPVAFPTTERLIGMAAKNOVA 60
DB	1	MAKAAAGIDIGTTCVGVFQHGKVEIIANDGNGRTTSPVAFPTTERLIGMAAKNOVA 60
QY	61	LNPONTVFDAKRLIGRRKFGDPVVOQSDMKHWPFOVINDGDKPKVOVSYKGTAKAFYEIS 120
DB	61	LNPONTVFDAKRLIGRRKFGDPVVOQSDMKHWPFOVINDGDKPKVOVSYKGTAKAFYEIS 120

QY 121 SMVLTKMEIAEAYLGYPVNAVITVPAYFNDSDQATKDAAGVLAGLVLRINEPTAAA 180  
DB 121 SMVLTKMEIAEAYLGYPVNAVITVPAYFNDSDQATKDAAGVLAGLVLRINEPTAAA 180  
QY 181 IAYGIDRFGKGERNVLIDLGCGTFDVSILTTIDGIFFEVKATAGDTHHGGEFDRNLVNH 240  
DB 181 IAYGIDRFGKGERNVLIDLGCGTFDVSILTTIDGIFFEVKATAGDTHHGGEFDRNLVNH 240  
QY 241 FVEEFKRKHKKDISQNKRAVRRLTACERAKRTLSSTQASLEIDSLEEGIDFYTSTRA 300  
DB 241 FVEEFKRKHKKDISQNKRAVRRLTACERAKRTLSSTQASLEIDSLEEGIDFYTSTRA 300  
QY 301 REELCSDLFRSTLEPEVEKALDKAKQIHDLVYVGSSTRIIPYQKLLDPFNGRDLN 360  
DB 301 REELCSDLFRSTLEPEVEKALDKAKQIHDLVYVGSSTRIIPYQKLLDPFNGRDLN 360  
QY 361 KININDEAVAYGAAYOALIMGDKSENVDLLDLVAPLSLGLTETAGVMTALIKRNSTI 420  
DB 361 KININDEAVAYGAAYOALIMGDKSENVDLLDLVAPLSLGLTETAGVMTALIKRNSTI 420  
QY 421 PKQOTIFFTYSDNPGVLIQVYEGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDI 480  
DB 421 PKQOTIFFTYSDNPGVLIQVYEGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDI 480  
QY 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOEAKYAEDEVQDRSAKN 540  
DB 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOEAKYAEDEVQDRSAKN 540  
QY 541 ALESYAFNMKSAVEDGLGKISEADKKRYLDKCOEIVISMLDANTLAERDEFHKKRELE 600  
DB 541 ALESYAFNMKSAVEDGLGKISEADKKRYLDKCOEIVISMLDANTLAERDEFHKKRELE 600  
QY 601 QVCNPIISGLYOGAGRGPGCGAGCPKGSSEGPITIEVD 641  
DB 601 QVCNPIISGLYOGAGRGPGCGAGCPKGSSEGPITIEVD 641  
RESULT 2  
Q9QWJ5 PRELIMINARY; PRT; 641 AA.  
AC Q9QWJ5; 09QWJ5;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE HSP70.  
GN H2-BF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RA Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R.,  
Schafter T., Ratcliffe A., Abbasi N., Loretz C., Laaky S., Hood L.,  
\*Sequence of the mouse MHC class III region.\*  
RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
DR EMBL: AF109906; AAC84169.1; -;  
DR HSSP: P08107; 1HJO.  
DR MGD: MGI:105975; H2-BF.  
DR InterPro: IPR001023; Hsp70.  
DR Pfam: PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PRODOM: PD000089; HSP70; 1.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW ATP-binding.  
SQ SEQUENCE 641 AA; 70079 MW; F49C33E602EAE334 CRC64;  
Query Match 96.1%; Score 3136; DB 11; Length 641;

Best Local Similarity 95.3%; Pred. No. 1,56-170;  
Matches 611; Conservative 20; Mismatches 10; Indels 0; Gaps 0;  
QY 1 MAKAAATIDIGTYSYCVGVHOGKVELIANDQGRKTPSYVAFDPRELRIGDAKKNYA 60  
DB 1 MAKNAATIDIGTYSYCVGVHOGKVELIANDQGRKTPSYVAFDPRELRIGDAKKNYA 60  
QY 61 LNPONTVDARKLIGRKGDPPVQSDMKHMPFOVYNDGDKPKVQVSYKGETKAFYPEEIS 120  
DB 61 LNPONTVDARKLIGRKGDPPVQSDMKHMPFOVYNDGDKPKVQVSYKGETKAFYPEEIS 120  
QY 121 SMVLTKMEIAEAYLGYPVNAVITVPAYFNDSDQATKDAAGVLAGLVLRINEPTAAA 180  
DB 121 SMVLTKMEIAEAYLGYPVNAVITVPAYFNDSDQATKDAAGVLAGLVLRINEPTAAA 180  
QY 181 IAYGIDRFGKGERNVLIDLGCGTFDVSILTTIDGIFFEVKATAGDTHHGGEFDRNLVNH 240  
DB 181 IAYGIDRFGKGERNVLIDLGCGTFDVSILTTIDGIFFEVKATAGDTHHGGEFDRNLVNH 240  
QY 241 FVEEFKRKHKKDISQNKRAVRRLTACERAKRTLSSTQASLEIDSLEEGIDFYTSTRA 300  
DB 241 FVEEFKRKHKKDISQNKRAVRRLTACERAKRTLSSTQASLEIDSLEEGIDFYTSTRA 300  
QY 301 REELCSDLFRSTLEPEVEKALDKAKQIHDLVYVGSSTRIIPYQKLLDPFNGRDLN 360  
DB 301 REELCSDLFRSTLEPEVEKALDKAKQIHDLVYVGSSTRIIPYQKLLDPFNGRDLN 360  
QY 361 KININDEAVAYGAAYOALIMGDKSENVDLLDLVAPLSLGLTETAGVMTALIKRNSTI 420  
DB 361 KININDEAVAYGAAYOALIMGDKSENVDLLDLVAPLSLGLTETAGVMTALIKRNSTI 420  
QY 421 PKQOTIFFTYSDNPGVLIQVYEGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDI 480  
DB 421 PKQOTIFFTYSDNPGVLIQVYEGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDI 480  
QY 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOEAKYAEDEVQDRSAKN 540  
DB 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOEAKYAEDEVQDRSAKN 540  
QY 541 ALESYAFNMKSAVEDGLGKISEADKKRYLDKCOEIVISMLDANTLAERDEFHKKRELE 600  
DB 541 ALESYAFNMKSAVEDGLGKISEADKKRYLDKCOEIVISMLDANTLAERDEFHKKRELE 600  
QY 601 QVCNPIISGLYOGAGRGPGCGAGCPKGSSEGPITIEVD 641  
DB 601 QVCNPIISGLYOGAGRGPGCGAGCPKGSSEGPITIEVD 641  
RESULT 3  
Q925V6 PRELIMINARY; PRT; 642 AA.  
AC Q925V6; 0925V6;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE HSP70.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RA Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R.,  
Schafter T., Ratcliffe A., Abbasi N., Loretz C., Laaky S., Hood L.,  
\*Sequence of the mouse MHC class III region.\*  
RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
DR EMBL: AF109906; AAC84168.1; -;  
DR InterPro: IPR001023; Hsp70.  
DR Pfam: PF00012; HSP70; 1.  
DR PRODOM: PD000089; HSP70; 1.  
DR PROSITE: PS00297; HSP70\_1; UNKNOWN\_1.

DR	PROSITE:	PS00329;	HSP70_2;	UNKNOWN_1.
DR	PROSITE:	PS01036;	HSP70_3;	UNKNOWN_1.
KW	ATP-binding.			
SO	SEQUENCE	642 AA;	70176 MW;	4BB9B0B130C23D8B CRC64

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA MEDLINE=985192; PubMed=9685725;
RA Ito Y., Ando A., Ando H., Ando J., Saijoh Y., Inoko H., Fujimoto H.;
RT "Genomic structure of the spermatid-specific HSP70 homolog gene
RT located in the class III region of the major histocompatibility
RT complex of mouse and man."
RL J. Biochem. 124:347-353(1998).
CC -1. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; D85730; BAA32521.1; -.
DR HSSP; P08107; HSP70.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; HSP70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock
KW SEQUENCE 641 AA; 70437 MW; 303385E7D43019F7 CRC64;
SQ
Query Match 89.6%; Score 2925; DB 4; Length 641;
Best Local Similarity 88.4%; Pred. No. 1.5e-158;
Matches 572; Conservative 34; Mismatches 25; Indels 16; Gaps 2;
OY 2 AKAAIGIDLGTTCSCVGFQHGKVEIIANDGNTTSSYVAFPTTERLIGDAKNQVAL 61
DB 4 AKGIAIGIDLGTTCSCVGFQHGKVEIIANDGNTTSSYVAFPTTERLIGDAKNQVAL 63
OY 62 NPQNTVPFAKRLIGRKFPDPPVQADMKLMPFQVINEGKPKVLVSYKGNKAFYEELSS 121
DB 64 NPQNTVPFAKRLIGRKFPDPPVQADMKLMPFQVINEGKPKVLVSYKGNKAFYEELSS 123
OY 122 MYLTAKKEIAEAYLGYPVTNAVITVPAYFNDQSQRATDAGYIAGLVLRITNEPTAAI 181
DB 124 MYLTAKKEIAEAYLGYPVTNAVITVPAYFNDQSQRATDAGYIAGLVLRITNEPTAAI 183
OY 182 AYGLDRGTGGERNVLIIFDLGGTFPVSLITDDGIFEVKATAGDTHLGEDPDNLVNH 241
DB 184 AYGLDRGTGGERNVLIIFDLGGTFPVSLITDDGIFEVKATAGDTHLGEDPDNLVNH 243
OY 242 VEEFRKRRKKDISOAKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITR 301
DB 244 VEEFRKRRKKDISOAKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITR 303
OY 302 FEELCSDFRSTLEVEKALDKAQIHDVLVYGSTRIPKVOKLLODFEFGNDLNK 361
DB 304 FEELCSDFRSTLEVEKALDKAQIHDVLVYGSTRIPKVOKLLODFEFGNDLNK 363
OY 362 SINPDEAVAYGAOVAALIMDGKSENVDLLLDVAPLSIGLETAGVMTALIKRNSITP 421
DB 364 SINPDEAVAYGAOVAALIMDGKSENVDLLLDVAPLSIGLETAGVMTALIKRNSITP 423
OY 422 TKQOIFFTYSDNPGVLIQYVEGERAMTKDNNLGRFELSGIPAPGVPQIETFPDID 481
DB 424 TKQOIFFTYSDNPGVLIQYVEGERAMTKDNNLGRFELSGIPAPGVPQIETFPDID 483
OY 482 ANGLINVTATKSTGKAKKITTNDKGRLSKEEIERVQAEKKADEDEVORERYSAKNA 541
DB 484 ANGLINVTATKSTGKAKKITTNDKGRLSKEEIERVQAEKKADEDEVORERYSAKNA 543
OY 542 LESTAFNNKSAVEDEGKLGKTSADKKVLDKQEVISMDANTLAEDDEFERKKELEQ 601
DB 544 LESTAFNNKSAVEDEGKLGKTSADKKVLDKQEVISMDANTLAEDDEFERKKELEQ 603
OY 602 VCNPIISGLYOGAGPGPGFGAOGPKGSG-----SGPTIEVD 641
DB 604 MGNPIITIKLYOG-----GCTGPACGTCGYMGRRATGPTIEVD 641
```

```
RESULT 6
ID 096OC9 PRELIMINARY; PRT; 641 AA.
AC 096OC9;
DT 01-DEC-2001 (TRENMBIrel. 19, Created)
DT 01-DEC-2001 (TRENMBIrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENMBIrel. 20, Last annotation update)
DE Heat shock protein.
GN HSPAL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirakawa M., Yamaguchi H., Imai K., Shinada J.;
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Shina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,812bp genomic DNA of 6p21.3 HLA class I region."
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -1. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AP00503; BAB3301.1; -.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRODOM; PD000089; HSP70_1.
DR PROSITE; PS00297; HSP70_1; UNKNOWN_1.
DR PROSITE; PS00329; HSP70_2; UNKNOWN_1.
DR PROSITE; PS01036; HSP70_3; UNKNOWN_1.
KW ATP-binding.
KW SEQUENCE 641 AA; 70405 MW; 303385E7D4300440 CRC64;
SQ
```

```
Query Match 89.6%; Score 2925; DB 4; Length 641;
Best Local Similarity 88.4%; Pred. No. 1.5e-158;
Matches 572; Conservative 34; Mismatches 25; Indels 16; Gaps 2;
OY 2 AKAAIGIDLGTTCSCVGFQHGKVEIIANDGNTTSSYVAFPTTERLIGDAKNQVAL 61
DB 4 AKGIAIGIDLGTTCSCVGFQHGKVEIIANDGNTTSSYVAFPTTERLIGDAKNQVAL 63
OY 62 NPQNTVPFAKRLIGRKFPDPPVQADMKLMPFQVINEGKPKVLVSYKGNKAFYEELSS 121
DB 64 NPQNTVPFAKRLIGRKFPDPPVQADMKLMPFQVINEGKPKVLVSYKGNKAFYEELSS 123
OY 122 MYLTAKKEIAEAYLGYPVTNAVITVPAYFNDQSQRATDAGYIAGLVLRITNEPTAAI 181
DB 124 MYLTAKKEIAEAYLGYPVTNAVITVPAYFNDQSQRATDAGYIAGLVLRITNEPTAAI 183
OY 182 AYGLDRGTGGERNVLIIFDLGGTFPVSLITDDGIFEVKATAGDTHLGEDPDNLVNH 241
DB 184 AYGLDRGTGGERNVLIIFDLGGTFPVSLITDDGIFEVKATAGDTHLGEDPDNLVNH 243
OY 242 VEEFRKRRKKDISOAKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITR 301
DB 244 VEEFRKRRKKDISOAKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITR 303
OY 302 FEELCSDFRSTLEVEKALDKAQIHDVLVYGSTRIPKVOKLLODFEFGNDLNK 361
DB 304 FEELCSDFRSTLEVEKALDKAQIHDVLVYGSTRIPKVOKLLODFEFGNDLNK 363
OY 362 SINPDEAVAYGAOVAALIMDGKSENVDLLLDVAPLSIGLETAGVMTALIKRNSITP 421
DB 364 SINPDEAVAYGAOVAALIMDGKSENVDLLLDVAPLSIGLETAGVMTALIKRNSITP 423
OY 422 TKQOIFFTYSDNPGVLIQYVEGERAMTKDNNLGRFELSGIPAPGVPQIETFPDID 481
DB 424 TKQOIFFTYSDNPGVLIQYVEGERAMTKDNNLGRFELSGIPAPGVPQIETFPDID 483
OY 482 ANGLINVTATKSTGKAKKITTNDKGRLSKEEIERVQAEKKADEDEVORERYSAKNA 541
DB 484 ANGLINVTATKSTGKAKKITTNDKGRLSKEEIERVQAEKKADEDEVORERYSAKNA 543
```



QY	542	LESYAFNNKSAVEDSGLKGTISEAKKKVYLKDCQVIVSLWANTLANLAEKDFPHKKRELEQ	601
DB	544	LESYAFNNKSAVSDGKLGKGTISEQKKNLTLDCNELLSELVNOIALEKDFPHKKRELEQ	603
QY	602	VCPNPIISGLYOGAGGPGGFGAOGPKKSGS-----SGPIFEYVD	641
DB	604	MCNPILITLXYGS-----GCTGPAGCTGTVPRPATPIIEYVD	641
RESULT 7			
ID	088686	PRELIMINARY;	PRT; 641 AA.
AC	088686;		
DT	01-NOV-1998	(TREMBLrel. 08, Created)	
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)	
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)	
DE	Spermatid-specific heat shock protein 70.		
GN	HSPALL OR HSC70F.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RP	(1)		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=BAIB/C; TISSUE=TESTIS;		
EX	MEDLINE=98351992; PubMed=9685725;		
RA	Ito Y., Ando A., Ando H., Ando J., Saitoh Y., Inoko H., Fujimoto H.;		
RT	Genomic structure of the spermatid-specific HSP70 homolog gene		
RT	located in the class III region of the major histocompatibility		
RT	complex of mouse and man. *.		
RL	J. Biochem. 124:347-353(1998).		
CC	-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.		
DR	EMBL; D85732; BAA32522.1; -.		
DR	HSSP; P08107; IADO.		
DR	MCD; MGI:96231; Hspall.		
DR	InterPro: IPR001023; Hsp70.		
DR	Pfam: PF00012; HSP70.1		
DR	PRINTS: PR00301; HEATSHOCK70.		
DR	ProDom: PD000089; Hsp70; 1.		
DR	PROSITE: PS00297; HSP70.1; 1.		
DR	PROSITE: PS00329; HSP70.2; 1.		
DR	PROSITE: PS01036; HSP70.3; 1.		
KW	ATP-binding; Heat shock		
SEQ	SEQUENCE 641 AA; 70623 MW; D19B11742A03BC2F CRC64;		
Query Match 88.5%; Score 2889; DB 11; Length 641;			
Best Local Similarity 89.0%; Pred. NO. 1.7e-156;			
Matches 569; Conservative 32; Mismatches 36; Indels 2; Gaps 2			
QY	3	KAAAGIDGTTYSCGVYQHKGVELIANDQGNRTTPSYAATDPERLLIGDAKNOVALN	62
DB	5	KMAAGIDGTTYSCGVYQHKGVELIANDQGNRTTPSYAATDPERLLIGDAKNOVALN	64
QY	63	PONTFFDAKRLIGKRFQGDVYVQSDMKHMPFOYINDGDKRVQVSYKGFKAPEEISSM	122
DB	65	PQNTVFDAKRLIGKRFNDPVYVQSDMKLMPFOYINELGKRVVSYKGEKATPEEISSM	124
QY	123	VLTKKELAEAVLGVPTNAVTTPAYFNDSORATKDGAVTAGLVLRINIEPTAAALA	182
DB	125	VLTKKELAEAVLGHNVNNAVTTPAYFNDSORATKDGAVTAGLVLRINIEPTAAALA	184
QY	183	YGLDGTGGERVVLFFDGGGFEVDSILTDIGIFEVKATPADTHLGGEDPNRLVNHVY	242
DB	185	YGLDGTGGERVVLFFDGGGFEVDSILTDIGIFEVKATPADTHLGGEDPNRLVSHVY	244
QY	243	EEFKRHKKDISQNRRAVRLRTACEERAKRTLSSSTOASLEDSLEFGIDFTYSITRAF	302
DB	245	EEFKRHKKDISQNRRAVRLRTACEERAKRTLSSSTOAMLEIDSLYEGIDFTYSITRAF	304
QY	303	EELCSDLFRSTLEPEPEKALROAKLDKAQIHDVLVYGGSTRIRKRVOKLDDFNGRLNKS	362
DB	305	EELCADLRGTLTEPEKSLROAKMDKAKIHDIVLVGGSTRIRKRVOKLDDYNGRLNKS	364

QY	363	INPDDAVAYGA	VAQAAILLMGDKSENVODILLIDVAPLSIGLETFACGVMATLKRNSTIPT	422			
QY	364	INPDDAVAYGA <td>VAQAAILLMGDKSENVODILLIDVAPLSIGLETFACGVMATLKRNSTIPT</td> <td>422</td>	VAQAAILLMGDKSENVODILLIDVAPLSIGLETFACGVMATLKRNSTIPT	422			
Db	365	INPDDAVAYGA <td>VAQAAILLMGDKSENVODILLIDVAPLSIGLETFACGVMATLKRNSTIPT</td> <td>424</td>	VAQAAILLMGDKSENVODILLIDVAPLSIGLETFACGVMATLKRNSTIPT	424			
QY	423	KOTQLEFYYSDNQ	PGLVLIQVYEGERAMTFKDNMLGSRFELSGIPPAAPRGVQJLEVFDDIDA	482			
Db	425	KOTQLEFYYSDNQ	PGLVLIQVYEGERAMTRDNMLGSRFELSGIPPAAPRGVQJLEVFDDIDA	484			
QY	483	NCILNVAATDKSTG	KRANKTTITNDKGRSLKEEIERMVAEAEKYKADEYQREBRVSAKNAL	542			
Db	485	NCILNVAATDKSTG	KRANKTTITNDKGRSLKEEIERMVAEAEKYKADEYQREBRVSAKNAL	544			
QY	543	ESYAANMMSAV	DEGLKAGISADKKVYLDKQOEYISMLDANTLAKDEFEKREKRELECY	602			
Db	545	ESYAANMMSAV	DEGLKAGISADKKVYLDKQOEYISMLDANTLAKDEFEKREKRELECY	604			
QY	603	CNPITISGLYQAG	GCGGFGAQCQKGGSGSGPTTIEEVD	641			
Db	605	CNPITITKLKYG	-SGCTGPTCTPGYTP-GRATGPTTIEEVD	641			
RESULT 8							
QY	08UY14	PRELIMINARY: PRT: 651 AA.					
AC	08UY14						
DT	01-MAR-2002	(TREMBlrel. 20, Created)					
DT	01-MAR-2002	(TREMBlrel. 20, Last sequence update)					
DT	01-JUN-2002	(TREMBlrel. 21, Last annotation update)					
DE	Heat shock protein 70.						
GN	HSP70.						
OS	Ampyostoma mexicanum (Axolotl).						
OC	Euryarchaea, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;						
OC	Ambystoma.						
OX	NCBI_TaxID=8296;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Ordonez M.R., Pichon L.L., Laurens V.;						
RT	"Characterization of a cDNA encoding a member of the heat shock 70KD						
RT	protein family (HSP70) in axolotl.";						
RL	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.						
DR	EMBL: AY029210; AAK31583.1;						
DR	InterPro: IPR001023; HSP70.						
DR	Pfam: PF00012; HSP70.1.						
DR	PRINTS: PR00301; HEATSHOCK70.						
DR	ProDom: PD000089; HSP70.1.						
DR	PROSITE: PS00297; HSP70.1; UNKNOWN.1.						
DR	PROSITE: PS00329; HSP70.2; UNKNOWN.1.						
DR	PROSITE: PS01036; HSP70.3; UNKNOWN.1.						
SO	SEQUENCE 651 AA; 71055 MW; 86c73fRa0DCEFCB9D CRC64;						
Query Match							
Best Local Similarity		86.7%;	Score 2829;	DB 13; Length 651;			
Matches 553; Conservative		46;	Pred: No. 4.6e-153;				
			Mismatches 42;	Indels 10; Gaps			
QY	1	MAKAAATGIDGIDT	TSVCVGFPOHGAKEVETIANQGNRTTTSYAFPTDTELIDDAKNQYA	60			
Db	1	MSKGSVGGIDGIDT	TSVCVGFPOHGAKEVETIANQGNRTTTSYAFPTDTELIDDAKNQYA	60			
QY	61	LNPNQVFPDAKRL	IGKRFEDPVVQSDMKMPFOVINDDGKPKVQVYSKYCKETAFYEETIS	120			
Db	61	MAPPTNVFPAKRL	IGKRFEDGVVQSDMKMPFNVISDGRPRVQVDYKQETSFYEBS	120			
QY	121	SNVLTKMKELIAP	YLGYPVTAIVTPAYFENDSQRAATKDACVAGLNLVRIITNEPTAA	180			
Db	121	SNVLTKMKELIAP	YLGKTVSNVAVTPAYFENDSQRAATKDACVAGLNLVRIITNEPTAA	180			
QY	181	IAYGIDRNGKGR	NRNVLIPIGLGGTDPVSLITLIDGIFFEVKATAGPHILGGEDFNRLVNH	240			
Db	181	IAYGIDRNGKGR	NRNVLIPIGLGGTDPVSLITLIDGIFFEVKATAGPHILGGEDFNRLVNH	240			
QY	241	FVEEFRRKKRKK	DISQNRKAVRRLTFACEAKRTLSSTQASLETISLFGIDIFYTSITRA	300			

[illegible]

Query Match	86.6%	Score 2826.5	DB 13	Length 646
Best Local Similarity	84.8%	Pred. No. 6.3e-153		
Matches 548	Conservative 48	Mismatches 45	Indels 5	Gaps 3
QY 1	MAKAAAGIDIGTGYSCVGFQHGKVELIANDQGNRTTPTSYVAFDTERLIGDAKNOVA	60		
DB 1	MSKGAIVGIDIGTGYSCVGFQHGKVELIANDQGNRTTPTSYVAFDTERLIGDAKNOVA	60		
QY 61	LNPNQTVDAKRLIGRKRGDPVYOSDMKHFPVOYINDGDKRVQVSTGFKATPEEIS	120		
DB 61	MLPPTVVDARLIGRRPDDSVOSDMKHFPVTYVNDAGRKVQVVEYKGETKSPYEIS	120		
QY 121	SMVLTKMEIEAAYLGYPVNAVITVPYEFNDOSROAKDKDGVLAGLVLTINEPTAAA	180		
DB 121	SMVLTKMEIEAAYLGKTYVNAVITVPYEFNDOSROAKDKDGVLAGLVLTINEPTAAA	180		
QY 181	IAYGIDRTGKKEBNVLFDLGGGTFDVSILTTDDGIFEVKATAGDTHLGGEDFNNRLVNH	240		
DB 181	IAYGIDRTGKKEBNVLFDLGGGTFDVSILTTDDGIFEVKATAGDTHLGGEDFNNRLVNH	240		
QY 241	FVEEKKRKHKKDISONKRAVRLRTRACRARRTSSSTQASLEIDSLEEGIDFTTSTIRA	300		
DB 241	FVEEKKRKHKKDISONKRAVRLRTRACRARRTSSSTQASLEIDSLEEGIDFTTSTIRA	300		
QY 301	RPEELCSLFPSTLEPEVKALNDALDKAOLHDLVLVGGSTRIRPVOKLDDPFNGRDLN	360		
DB 301	RPEELCSLFPSTLEPEVKALNDALDKAOLHDLVLVGGSTRIRPVOKLDDPFNGRDLN	360		
QY 361	KSINDEAVAVGAOVAAILMGDKSENVQDILLDVPALSLGLETAGCVMTALIKRNSTI	420		
DB 361	KSINDEAVAVGAOVAAILMGDKSENVQDILLDVPALSLGLETAGCVMTALIKRNSTI	420		
QY 421	PTKOTQITFTTYSNDNPGVLIOYBGERAMTKDNLLGFELSGIPAPRGVQJIEVTFDI	480		
DB 421	PTKOTQITFTTYSNDNPGVLIOYBGERAMTKDNLLGFELSGIPAPRGVQJIEVTFDI	480		
QY 481	DANGLINTATDUSGKRNKLTITNDKGRLSKEEIERVQVAEYKKADEYQREKRVSKN	540		
DB 481	DANGLINTATDUSGKRNKLTITNDKGRLSKEEIERVQVAEYKKADEYQREKRVSKN	540		
QY 541	ALESAFAFNKSAVEDEGEGKRISEADKKKVLDDCOEVSMLDANTLTAEKDEPHEKRIELE	600		
DB 541	SLSDSAFAFNKSAVEDEGEGKRISEADKKKVLDDCOEVSMLDANTLTAEKDEPHEKRIELE	600		
QY 601	QVCNPIISGLYOGAGG-PG--PGGF--GAGGPKGSGSGSPRIIEYVD 641			
DB 601	KVCNPIITFKLYOGAGGMPGMPGCGPGCGAPPSCGASGSPRIIEYVD 646			
RESULT 10				
073922				
ID 073922	PRELIMINARY;	PRT;	639 AA.	
AC 073922				
DT 01-AUG-1998	(TREMblrel. 07, created)			
DT 01-AUG-1998	(TREMblrel. 07, last sequence update)			
DT 01-MAR-2002	(TREMblrel. 20, last annotation update)			
DE	Heat shock protein 70.			
GN	HSP70.			
OS	Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorphi; Acanthopterygii; Percomorphi; Perciformes; Labroidel;			
OC	Cichlidae; Oreochromis.			
OX	NCBI_TaxID=8127;			
RN	111			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20291068; PubMed=10828441;			
RA	Molina A., Blemer F., Mueller F., Iyengar A., Prunet P., Maclean N.,			
RA	Martini J.A., Miller M.;			
RT	"Cloning and expression analysis of an inducible HSP70 gene from			
RT	tilapia fish";			
RL	FEBS Lett. 474:5-10(2000).			
CC	-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.			

DR EMBL: AJ001312; CAA04673.1; -  
 DR HSSP: P08109; ICKR.  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PRODOM: PD000089; Hsp70; 1.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR APP-binding.  
 KW SEQUENCE 639 AA; 70292 MW; B269FA98407BD4AE CRC64;

Query Match 86.4%; Score 2820.5; DB 13; Length 639;  
 Best Local Similarity 85.8%; Pred. No. 14e-152;  
 Matches 548; Conservative 47; Mismatches 41; Indels 3; Gaps 2;

QY 3 KAAAGIDLTGTTSCVGVFQHGKVEIIANDOGNRTTPSYAFDTERLIGDAKNOVALN 62  
 DB 4 KGAAGIDLTGTTSCVGVFQHGKVEIIANDOGNRTTPSYAFDTERLIGDAKNOVALN 63  
 QY 63 PONTVFPAKRLIGKFGDPVVOGSMKHPROYINDGKPKVOYSKGETAFPEEISSM 122  
 DB 64 PSNTVFPAKRLIGKFGDPVVOGSMKHPROYINDGKPKRVEYKGEKAFPEEISSM 123  
 QY 123 VLTAKKEIAEAYLGYPYTNNAVITPAYFENDSORQATKDAGYIAGLVRLIINEPTAAIA 182  
 DB 124 VLVAKKEIAEAYLGQKYSNAVITPAYFENDSORQATKDAGYIAGLVRLIINEPTAAIA 183  
 QY 183 YGLDRTGKGERNVLIIFDLGGTFPVSLITIDGIFEYKATAGDTHLGGEDENRLVNHFV 242  
 DB 184 YGLDKGSGERNVLIIFDLGGTFPVSLITIDGIFEYKSTAGDTHLGGEDENRNVNHFV 243  
 QY 243 EEFRKHKKDISOKKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFYTSTTRARF 302  
 DB 244 EEFRKHKKDISOKKRALRLTAERAKRTLSSSQASLEIDSLFEGVDFTSTTRARF 303  
 QY 303 EELCSDFRSTLEPEVEKALRDADKAQIHDLVVGSTRIPKYOKLQDFPFGRLNKS 362  
 DB 304 EELCSDFRSTLEPEVEKALRDADKAQIHDLVVGSTRIPKYOKLQDFPFGRLNKS 363  
 QY 363 INPDEAVAYGAOVAAILMGDSKNVODLLLDVAPLSLGETAGVMTALIKRNSTIPT 422  
 DB 364 INPDEAVAYGAOVAAILMGDSKNVODLLLDVAPLSLGETAGVMTALIKRNSTIPT 423  
 QY 423 KOTQIFFTYSNONGVLIQYVEGERAMTKDNLLGREFLSIIPAPRGVQIETVFDIDA 482  
 DB 424 KOTQIFFTYSNONGVLIQYVEGERAMTKDNLLGREFLSIIPAPRGVQIETVFDIDA 483  
 QY 483 NGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYKAEDVORERVSANKAL 542  
 DB 484 NGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYKAEDVORERVSANKAL 543  
 QY 543 ESYAFNMKSAVEDGLKGLKISEADKKVLDKQEVISMLDANTLAENDEFBHKRELEQV 602  
 DB 544 ESYAFNMKSSVQDNLNKKIISEEDKKRYVEKDEALIAWLNQJLADREYOHKQELEKV 603  
 QY 603 CNPITISGLYOGAGGPGFGAGCPKGGSGSGPTTEEVD 641  
 DB 604 CNPITISGLYOGAGGPGFGAGCPKGGSGSGPTTEEVD 639

RESULT 11  
 093240 PRELIMINARY; PRT: 640 AA.  
 AC 093240;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE HSP70  
 OS Paralicthys olivaceus (Flounder).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopteleostei; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

OC Pleuronectoidae; Paralicthidae; Paralicthys.  
 OX NCBI\_TaxID=8255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yokoyama Y., Hashimoto H., Kubota S., Kinoshita M., Toyohara H.,  
 RA Sakaguchi M., Tanaka M., Seikai T., Kanamori M.,  
 RT "cDNA Cloning of Heat-Inducible HSP70, a 70.6 kDa Heat Shock Protein,  
 RT in Japanese Flounder Paralicthys olivaceus.";  
 RL Fisheries Sci. 0:0-0(1998).  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL: AB010871; BAA31697.1; -  
 DR HSSP: P08107; HSO.  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PRODOM: PD000089; Hsp70; 1.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR APP-binding  
 KW SEQUENCE 640 AA; 70608 MW; 9C8E65738FC0CF705 CRC64;

Query Match 85.8%; Score 2800.5; DB 13; Length 640;  
 Best Local Similarity 84.2%; Pred. No. 1.9e-151;  
 Matches 539; Conservative 59; Mismatches 39; Indels 3; Gaps 2;

QY 2 AKAAGIDLTGTTSCVGVFQHGKVEIIANDOGNRTTPSYAFDTERLIGDAKNOVAL 61  
 DB 4 AKGISIGIDLTGTTSCVGVFQHGKVEIIANDOGNRTTPSYAFDTERLIGDAKNOVAL 63  
 QY 62 PONTVFPAKRLIGKFGDPVVOGSMKHPROYINDGKPKVOYSKGETAFPEEISS 121  
 DB 64 PSNTVFPAKRLIGKFGDPVVOGSMKHPROYINDGKPKRVEYKGEKAFPEEISS 123  
 QY 122 VLTAKKEIAEAYLGYPYTNNAVITPAYFENDSORQATKDAGYIAGLVRLIINEPTAAI 181  
 DB 124 VLVAKKEIAEAYLGQKYSNAVITPAYFENDSORQATKDAGYIAGLVRLIINEPTAAI 183  
 QY 182 YGLDRTGKGERNVLIIFDLGGTFPVSLITIDGIFEYKATAGDTHLGGEDENRLVNHF 241  
 DB 184 YGLDKGSGERNVLIIFDLGGTFPVSLITIDGIFEYKATAGDTHLGGEDENRNVNHF 243  
 QY 242 VEEFRKHKKDISOKKRAVRRLRTACERAKRTLSSSQASLEIDSLFEGIDFYTSTTRAR 301  
 DB 244 LEEFRKHKKDISOKKRAVRRLRTACERAKRTLSSSQASLEIDSLFEGIDFYTSTTRAR 303  
 QY 302 EELCSDFRSTLEPEVEKALRDADKAQIHDLVVGSTRIPKYOKLQDFPFGRLNKS 361  
 DB 304 EELCSDFRSTLEPEVEKALRDADKAQIHDLVVGSTRIPKYOKLQDFPFGRLNKS 363  
 QY 362 SINPDEAVAYGAOVAAILMGDSKNVODLLLDVAPLSLGETAGVMTALIKRNSTIPT 421  
 DB 364 SINPDEAVAYGAOVAAILMGDSKNVODLLLDVAPLSLGETAGVMTALIKRNSTIPT 423  
 QY 422 TKQOIFFTYSNONGVLIQYVEGERAMTKDNLLGREFLSIIPAPRGVQIETVFDIDA 481  
 DB 424 TKQOIFFTYSNONGVLIQYVEGERAMTKDNLLGREFLSIIPAPRGVQIETVFDIDA 483  
 QY 482 ANGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYKAEDVORERVSANKA 541  
 DB 484 ANGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYKAEDVORERVSANKA 543  
 QY 542 LESYAFNMKSAVEDGLKGLKISEADKKVLDKQEVISMLDANTLAENDEFBHKRELEQ 601  
 DB 544 LESYAFNMKSSVQDNLNKKIISEEDKKRYVEKDEALIAWLNQJLADREYEHQELEK 603  
 QY 602 VCNPIISGLYOGAGGPGFGAGCPKGGSGSGPTTEEVD 641  
 DB 604 VCNPIISGLYOGAGGPGFGAGCPKGGSGSGPTTEEVD 640

RESULT 12  
 08UNM9

```

ID 080MM9 PRELIMINARY; PRT; 639 AA.
AC 080MM9;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Stress protein HSP70-2.
GN HSP70-2.
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_Taxid=8083;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamashita M.;
RT "Characterization of multiple members of the HSP70 family in platyfish
RT cultured cells."
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062114; BAB72168.1; -.
DR InterPro: IPR001023; Hsp70.
DR Pfam: PF00012; HSP70.1
DR PRINTS: PR00301; HEATSHOCK70.
DR PRODOM: PD000089; Hsp70.1.
DR PROSITE: PS00297; HSP70_1; UNKNOWN_1.
DR PROSITE: PS00329; HSP70_2; UNKNOWN_1.
SQ SEQUENCE 639 AA; 70128 MW; 87382f59fde5532c CRC64;

```

```

Query Match 85.7%; Score 2798; DB 13; Length 639;
Best Local Similarity 84.2%; Pred. No. 2,6e-151;
Matches 539; Conservative 52; Mismatches 45; Indels 4; Gaps 1;

```

```

QY 2 AKAAIGIDGTTSCVGFQHGKVEIIANDGRTTPSYVATDTERLIGDAKNOVAL 61
DB 4 AKVAIGIDGTTSCVGFQHGKVEIIANDGRTTPSYVATDTERLIGDAKNOVAL 63
QY 62 NPONTVFDAKRLIGKFGDPVQSDMKHWPFOYINDGDKPKVOYSYKGETKAFYPEEIS 121
DB 64 NPNTVFDAKRLIGKFGDPVQSDMKHWPFOYINDGDKPKVOYSYKGETKAFYPEEIS 123
QY 122 MVLTKKKEIAEALGYPVNAVITVPAYFNDGSRQATKAGVYAGLVLRILNEPTAAAI 181
DB 124 MVLTKKKEIAEALGYPVNAVITVPAYFNDGSRQATKAGVYAGLVLRILNEPTAAAI 183
QY 182 AVGLDRTGGERNVLLIFDLGGTFDVSILITIDGIFEVATAGDTLGGEDDNRVLNHF 241
DB 184 AVGLDRTGGERNVLLIFDLGGTFDVSILITIDGIFEVATAGDTLGGEDDNRVLNHF 243
QY 242 VEEFKRHKKDISONKRAVRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRAR 301
DB 244 VEEFKRHKKDISONKRAVRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRAR 303
QY 302 FEEELGDLFRSTLEPEVKALRDAAKIDKAOIHDLVYGGSTRIPKVOKLLODFPNGDLAK 361
DB 304 FEEELGDLFRSTLEPEVKALRDAAKIDKAOIHDLVYGGSTRIPKVOKLLODFPNGDLAK 363
QY 362 SINDEAVAYGAQAAILMGDKSENVODLLLDVAPLSLGLETAGGVMTALIKRNTIP 421
DB 364 SINDEAVAYGAQAAILMGDKSENVODLLLDVAPLSLGLETAGGVMTALIKRNTIP 423
QY 422 TQOTQITFTTYSNDQPGVLIQVYEGERAMTKDNNLGRFELSGITPPARGVPQIEVTFDI 481
DB 424 TQOTQITFTTYSNDQPGVLIQVYEGERAMTKDNNLGRFELSGITPPARGVPQIEVTFDI 483
QY 482 ANGIILVNTATDSTGKANKITITNDKGRSKREIERMVOEAKYKAEDVOGERYSAKNA 541
DB 484 ANGIILVNTATDSTGKANKITITNDKGRSKREIERMVOEAKYKAEDVOGERYSAKNA 543
QY 542 LESYVFNKMSAVEDEGLKISEADKKVLYDCQEVISWLDANTLAEKDEFEHKKRELEO 601
DB 544 LESYVFNKMSAVEDEGLKISEADKKVLYDCQEVISWLDANTLAEKDEFEHKKRELEO 603
QY 602 VCNPIISLNGXGAGPGPGFGAOGPKGSGSGPTIEEVD 641

```

```

DB 604 VCNPIISLNGXGAGPGPGFGAOGPKGSGSGPTIEEVD 639

```

```

RESULT 13
ID 073788 PRELIMINARY; PRT; 650 AA.
AC 073788;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE Heat shock protein 70.
GN HSP70.
OS Parachanna olivacea (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Parachannidae; Parachannidae.
OX NCBI_Taxid=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim W.O., Lee J.H., Kim K.K., Lee S.J., Kang H.S., Kim H.D.;
RT "Molecular cloning and characterization of a heat shock protein 70-
RT related cDNA from olive flounder (Parachanna olivacea)."
RL Han-gul Yangsig Hag-hoeji 12:91-100(1999).
CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF053059; AAC38859.1; -.
DR HSP; P19120; IATR.
DR InterPro: IPR001023; Hsp70.
DR Pfam: PF00012; HSP70.1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PRODOM: PD000089; Hsp70.1.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 650 AA; 71115 MW; 6B24E7D409FC76EA CRC64;

```

```

Query Match 85.6%; Score 2792.5; DB 13; Length 650;
Best Local Similarity 83.4%; Pred. No. 5.5e-151;
Matches 542; Conservative 49; Mismatches 50; Indels 9; Gaps 3;

```

```

QY 1 MAKAAIGIDGTTSCVGFQHGKVEIIANDGRTTPSYVATDTERLIGDAKNOVA 60
DB 1 MKKGAAGVIGDITTSVGVFQHGKVEIIANDGRTTPSYVATDTERLIGDAKNOVA 60
QY 61 LNPQNTVFDAKRLIGKFGDPVQSDMKHWPFOYINDGDKPKVOYSYKGETKAFYPEEIS 120
DB 61 NPNTVFDAKRLIGKFGDPVQSDMKHWPFOYINDGDKPKVOYSYKGETKAFYPEEIS 120
QY 121 SMVLTKKKEIAEALGYPVNAVITVPAYFNDGSRQATKAGVYAGLVLRILNEPTAAAI 180
DB 121 SMVLTKKKEIAEALGYPVNAVITVPAYFNDGSRQATKAGVYAGLVLRILNEPTAAAI 180
QY 181 IAYGLDRTGGERNVLLIFDLGGTFDVSILITIDGIFEVATAGDTLGGEDDNRVLNHF 240
DB 181 IAYGLDRTGGERNVLLIFDLGGTFDVSILITIDGIFEVATAGDTLGGEDDNRVLNHF 240
QY 241 FVEEFKRRHKKDISONKRAVRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300
DB 241 FVEEFKRRHKKDISONKRAVRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300
QY 301 FEEELGDLFRSTLEPEVKALRDAAKIDKAOIHDLVYGGSTRIPKVOKLLODFPNGDLAK 360
DB 301 FEEELGDLFRSTLEPEVKALRDAAKIDKAOIHDLVYGGSTRIPKVOKLLODFPNGDLAK 360
QY 361 SINDEAVAYGAQAAILMGDKSENVODLLLDVAPLSLGLETAGGVMTALIKRNTIP 420
DB 361 SINDEAVAYGAQAAILMGDKSENVODLLLDVAPLSLGLETAGGVMTALIKRNTIP 420
QY 421 PTQOTQITFTTYSNDQPGVLIQVYEGERAMTKDNNLGRFELSGITPPARGVPQIEVTFDI 480
DB 421 PTQOTQITFTTYSNDQPGVLIQVYEGERAMTKDNNLGRFELSGITPPARGVPQIEVTFDI 480

```



QY	63	PONTFEDKRLIGRREGPVQVQSMKIHMPPOVIDGKPRVQVSYKETEAFPEELISSM	1222
Db	65	PNNYFQAKRLIGRREDDPVQSDMKHSEFVYSDGKPRVAYEHKEKNTFNPDEISSM	1244
QY	123	VLTKKELAEAYILCYPUTNAVITYPAYFENDSQOATDAGVLAGLVRLIINEPTAAIA	1822
Db	125	VLYKKELAEAYLQOQVTNAVITYPAYFENDSQOATDAGVLAGLVRLIINEPTAAHP	1844
QY	183	YGLDRGTGGENVNLIFDLGGSTFVYSILTDGJFEYKATAGDTHLGGEDFNLVNHFV	2422
Db	185	YGLDRKGSSENNVLIIFDLGGSTFVYSILTDGJFEYKATAGDTHLGGEDFNRMVNHFV	2444
QY	243	EEFKRHKHKKDISOKKRAVRRRLRTACERAKRTLSSSTQASLEIDSLEFGIDPYSTPRAR	3022
Db	245	EEFKRHKHKKDISOKKRALRLRLTACERAKRTLSSSSQASLEIDSLVYEGIDPYSTPRAR	3044
QY	303	EELCSDLEFRSTLEBEVEKALRPAKLDKAOIHLYVVGSGSTRIPYOKLLODFPNGRDLKS	3622
Db	305	EELCSDLEFRGLDVEYKALRPAKMDKQOIHDIYLVGSGSTRIPKLOKLLDFPNRELKNS	3644
QY	363	INPDEAVAYGAVAOAAIILMGDKSENVODLLLDVAPLSLGLTAGVYVALIKRNSITPT	4222
Db	365	INPDEAVAYGAVAOAAIILMGDTSENVODLLLDVAPLSLGLTAGVYVALIKRNTIPT	4244
QY	423	KOTQFTTYSNOCVULLQVYEGGRATKRONNLLGRELSGIRPAPRGVQIETPTIDA	4822
Db	425	KOTQFTTYSNOCRVULLQVEGGRATKRONNLLGKRELGIIPAPRGVQIETPTIDA	4844
QY	483	NGILNVATDSTCKRANKITTTNDKGRSLSEKELERMWQAEKYAEDVORERSAKNAL	5422
Db	485	NGILNVASADSKOKNTITTTNDKGRSLSEKELERMWQOEDPMYKAEEDLQREKISAKNSL	5444
QY	543	ESYAFNMKSAVEDBGLGKISEADKKRYVLDCOEIVISMLDANTLAEKDEFEHKRKELEQV	6022
Db	545	ESYAFNMKSSYEDONLKGKISEEDKKRYIEKCNVAEWLENNQADLADKEEYHOLKELEY	6044
QY	603	CNPIISGLYOGAGGPRGGRGAQPRGGSG---SGPIIE 638	
Db	605	CNPVISKLYO---GGMPAGGGCAQ--KASGSGALRGPLK 640	

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: December 4, 2002, 16:40:37 ; Search time 21 Seconds

(Without alignments)  
2934.389 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 3263  
Sequence: 1 MAKAAAGIDLGTTTSCVGV.....FGAOGPKGSGSGFTIEVD 641Scoring table: BIOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

PIR\_73:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
	1	3263	100.0	641	2	A45871
	2	3242.5	99.4	640	2	A29160
	3	3216	98.6	641	2	S53357
	4	3182	97.5	641	2	S35718
	5	3169	97.1	641	2	S54542
	6	3148.5	96.5	638	2	S31766
	7	3125.5	95.8	642	2	JH0095
	8	2921	89.5	641	2	B45871
	9	2894	88.7	641	2	S41415
	10	2882	88.3	641	2	S41415
	11	2862.5	87.7	646	2	S07197
	12	2862.5	87.7	646	2	JC4853
	13	2859.5	87.6	646	2	A27077
	14	2856.5	87.5	646	2	S31716
	15	2856.5	87.5	646	2	A45935
	16	2853.5	87.5	650	2	S11456
	17	2843.5	87.1	646	2	A35922
	18	2835.5	86.9	647	1	HMXL70
	19	2816	86.3	651	2	S21175
	20	2800.5	85.8	640	2	T43724
	21	2798	85.7	639	2	S25585
	22	2772.5	85.0	639	2	A55719
	23	2766	84.8	645	2	S15129
	24	2762	84.6	634	2	A25646
	25	2757.5	84.5	633	2	S10859
	26	2751.5	84.3	633	2	S08211
	27	2747	84.2	643	2	S09036
	28	2735	83.8	644	2	A45635
	29	2730.5	83.7	640	2	T21394

30	2716	83.2	651	2	A36333	dnak-type molecule
31	2670.5	81.8	654	2	S37004	dnak-type molecule
32	2664	81.6	641	2	JN0668	dnak-type molecule
33	2658.5	81.5	640	1	HNK7A	dnak-type molecule
34	2614	80.1	637	2	A48469	dnak-type molecule
35	2565.5	78.6	640	2	T43730	dnak-type molecule
36	2563	78.5	645	2	JC5642	dnak-type molecule
37	2552.5	78.2	647	2	T45522	heat shock protein
38	2528.5	77.5	651	2	JC4786	dnak-type molecule
39	2527.5	77.5	651	2	T45517	heat shock protein
40	2527	77.4	647	2	T41121	heat shock protein
41	2519.5	77.2	651	2	S03250	dnak-type molecule
42	2514.5	77.1	644	2	S67431	dnak-type molecule
43	2513.5	77.0	651	2	T48271	dnak-type molecule
44	2511.5	77.0	651	2	S46302	dnak-type molecule
45	2502.5	76.7	649	2	S53126	dnak-type molecule

## ALIGNMENTS

## RESULT 1

A45871

dnak-type molecular chaperone HSP70-1 - human  
N:Alternate names: heat shock protein HSP70-1C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 20-Aug-1999

C:Accession: A45871

R:Miller, C.M.; Campbell, R.D.  
Immunogenetics 32, 242-251, 1990

A:Title: Structure and expression of the three MHC-linked HSP70 genes.

A:Reference number: A45871; MUID:91055806; PMID:1700760

A:Accession: A45871

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-641 &lt;MUI&gt;

A:Cross-references: GB:M59828; GB:M34267; NID:g188487; PIDN:AAA63226.1; PID:g188488;

A:Description: Involved in protein folding and assembling/disassembling of protein co

A:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match	Query Similarity	Score	DB 2:	Length	641:
Best Local	Similarity	100.0%	Pred. No. 2e-172;		
Matches	641; Conservative	0;	Mismatches	0;	Indels
					Gaps
					0;
QY	1	MAKAAAGIDLGTTSCVGFQHKVEITANDQGNRTTSPYAFDTTERLIGDAKNQYA	60		
DB	1	MAKAAAGIDLGTTSCVGFQHKVEITANDQGNRTTSPYAFDTTERLIGDAKNQYA	60		
QY	61	LNPOVTVPDAKRLIGRKGGDPVYOSDMKHPVOVINDGKPRVOYSYKGETKAFYPEETS	120		
DB	61	LNPOVTVPDAKRLIGRKGGDPVYOSDMKHPVOVINDGKPRVOYSYKGETKAFYPEETS	120		
QY	121	SVVLTKMKETIAYVGYPTNAVITVPAYFNDSOQATDCAVINGLNVLRITINEPTAA	180		
DB	121	SVVLTKMKETIAYVGYPTNAVITVPAYFNDSOQATDCAVINGLNVLRITINEPTAA	180		
QY	181	IAYGLDRGKGRNVLIPLDGSGTFDVSILITIDDGIFEVKATAGDTHLGGEDFDRNLVNH	240		
DB	181	IAYGLDRGKGRNVLIPLDGSGTFDVSILITIDDGIFEVKATAGDTHLGGEDFDRNLVNH	240		
QY	241	FVEEERKRRKKKIDISONKRAVRRLRTACERAKTLLSSSTOASLEIDSLFEGIDFYSTR	300		
DB	241	FVEEERKRRKKKIDISONKRAVRRLRTACERAKTLLSSSTOASLEIDSLFEGIDFYSTR	300		
QY	301	REELICSDLFSTLEPVEKALDKAKIHDVIVGSGSTRIPVOKLIDOFPGRDIN	360		
DB	301	REELICSDLFSTLEPVEKALDKAKIHDVIVGSGSTRIPVOKLIDOFPGRDIN	360		
QY	361	KSINPDEAVAYGAOVAATIMGDKSENVODLLLDVAPLSLGLFTAGGVMTALIRNSTI	420		
DB	361	KSINPDEAVAYGAOVAATIMGDKSENVODLLLDVAPLSLGLFTAGGVMTALIRNSTI	420		

QY 421 PTKOTQIFTTYSDNQPCVLLIQVYEGGERAMTKDNNLLGRFELSGIPAPRGVPOLEVTEDI 480  
 DB 421 PTKOTQIFTTYSDNQPCVLLIQVYEGGERAMTKDNNLLGRFELSGIPAPRGVPOLEVTEDI 480  
 QY 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEIEEMVQEAERYKADEVOERERYSAKN 540  
 DB 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEIEEMVQEAERYKADEVOERERYSAKN 540  
 QY 541 ALBSYAFNMKSAVEDEGLKGISEADKKVLDKCOEYISWLDANTLAENKDEFHKRELE 600  
 DB 541 ALBSYAFNMKSAVEDEGLKGISEADKKVLDKCOEYISWLDANTLAENKDEFHKRELE 600  
 QY 601 QVCNPIISGLYOGAGPGPGFGAOGPKGSGSGPTIEYD 641  
 DB 601 QVCNPIISGLYOGAGPGPGFGAOGPKGSGSGPTIEYD 641

## RESULT 2

A29160  
 dnak-type: molecular chaperone HSPALL - human  
 N:Alternate names: heat shock protein, 70K  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Aug-1988 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
 C:Accession: A29160; 137561; 137562  
 R:Hunt, C.; Morimoto, R.I.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985  
 A:title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the m  
 A:Reference number: A29160; MUID:86016721; PMID:3931075  
 A:Accession: A29160  
 A:Molecule type: DNA  
 A:Residues: 1-640 <HUN>  
 A:Cross-references: GB:M11717; GB:M15432; NID:9184416; PIDN:AAA52697.1; PID:9386785  
 A:Note: the authors mistranslated residues 463, 491, and 492  
 R:Prabent, B.; Genthe, A.; Bennecke, B.J.  
 Nucleic Acids Res. 14, 8933-8948, 1986  
 A:title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepared f  
 A:Reference number: 137561; MUID:87066768; PMID:3786141  
 A:Accession: 137561  
 A>Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22 <RES>  
 A:Cross-references: EMBL:X04676; NID:933480; PIDN:CAA28391.1; PID:9332481  
 A:Accession: 137562  
 A>Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 616-640 <RE2>  
 A:Cross-references: EMBL:X04677; NID:932482; PIDN:CAA28382.1; PID:932483  
 C:Genetics:  
 A:Gene: GDB:HSPALL; HSP70-HOM  
 A:Cross-references: GDB:120058; OMIM:140559  
 A:Map position: 6p21.3-6p21.3  
 A:Introns: #status absent  
 C:Function:  
 A:Description: Involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 99.4%; Score 3242.5; DB 2; Length 640;  
 Best Local Similarity 99.5%; Pred. No. 2.7e-171;  
 Matches 638; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAKAAAIGIDLGTTYSCVGFQHGKVEIANDGKNRTTPSYAFTDTERLIGDAKNOVA 60  
 DB 1 MAKAAAIGIDLGTTYSCVGFQHGKVEIANDGKNRTTPSYAFTDTERLIGDAKNOVA 60  
 QY 61 LNPONTVFADKRLIGRKGDPVVOQSDMKHMPFOYINDGDKPKVOVSYKGETKAFYPEIS 120  
 DB 61 LNPONTVFADKRLIGRKGDPVVOQSDMKHMPFOYINDGDKPKVOVSYKGETKAFYPEIS 120  
 QY 121 SMVLTKKKEIAEAYLGVPTNNAVITVPAYFNDROKATKAGYAGLVLRILINEPTAAA 180  
 DB 121 SMVLTKKKEIAEAYLGVPTNNAVITVPAYFNDROKATKAGYAGLVLRILINEPTAAA 180

QY 181 IAYGLDRTGGERNVLLIFDLGGGTFDVSILTTIDGJFEVRAATAGDNLGGEFDNRLVNH 240  
 DB 181 IAYGLDRTGGERNVLLIFDLGGGTFDVSILTTIDGJFEVRAATAGDNLGGEFDNRLVNH 240  
 QY 241 FVEEFKRRHKKDISOKNRAVRRLTACERAKRLSSQSLSEIDSLFESIDRYTSTR 300  
 DB 241 FVEEFKRRHKKDISOKNRAVRRLTACERAKRLSSQSLSEIDSLFESIDRYTSTR 300  
 QY 301 RFEEICSDLRPSFLPEPERKALPAKLDKAOIHDLVLGSGSTRIPKVKLLQDFPNGLN 360  
 DB 301 RFEEICSDLRPSFLPEPERKALPAKLDKAOIHDLVLGSGSTRIPKVKLLQDFPNGLN 360  
 QY 361 KSINPDEAVAYGAOVAAILMGDSENVODLLLDVAPLSLGETAGVMTALIKRNTI 420  
 DB 361 KSINPDEAVAYGAOVAAILMGDSENVODLLLDVAPLSLGETAGVMTALIKRNTI 420  
 QY 421 PTKOTQIFTTYSDNQPCVLLIQVYEGGERAMTKDNNLLGRFELSGIPAPRGVPOLEVTEDI 480  
 DB 421 PTKOTQIFTTYSDNQPCVLLIQVYEGGERAMTKDNNLLGRFELSGIPAPRGVPOLEVTEDI 480  
 QY 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEIEEMVQEAERYKADEVOERERYSAKN 540  
 DB 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEIEEMVQEAERYKADEVOERERYSAKN 540  
 QY 541 ALBSYAFNMKSAVEDEGLKGISEADKKVLDKCOEYISWLDANTLAENKDEFHKRELE 600  
 DB 541 ALBSYAFNMKSAVEDEGLKGISEADKKVLDKCOEYISWLDANTLAENKDEFHKRELE 600  
 QY 601 QVCNPIISGLYOGAGPGPGFGAOGPKGSGSGPTIEYD 641  
 DB 601 QVCNPIISGLYOGAGPGPGFGAOGPKGSGSGPTIEYD 641

## RESULT 3

S53357  
 dnak-type: molecular chaperone hsp70 - bovine  
 N:Alternate names: 70K heat shock protein  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jul-2000  
 C:Accession: S53357  
 R:Gutierrez, J.A.; Guerriero Jr., V.  
 Biochem. J. 305, 197-203, 1995  
 A:title: Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-  
 A:Reference number: S53357; MUID:95126904; PMID:7826329  
 A:Accession: S53357  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-641 <GUT>  
 A:Cross-references: EMBL:U09861; NID:9497937; PIDN:AAA73914.1; PID:9497938  
 C:Genetics:  
 A:Gene: hsp70  
 C:Function:  
 A:Description: Involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock chaperone  
 C:Keywords: ATP; molecular chaperone

Query Match 98.6%; Score 3216; DB 2; Length 641;  
 Best Local Similarity 98.8%; Pred. No. 7.9e-170;  
 Matches 633; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAKAAAIGIDLGTTYSCVGFQHGKVEIANDGKNRTTPSYAFTDTERLIGDAKNOVA 60  
 DB 1 MAKAAAIGIDLGTTYSCVGFQHGKVEIANDGKNRTTPSYAFTDTERLIGDAKNOVA 60  
 QY 61 LNPONTVFADKRLIGRKGDPVVOQSDMKHMPFOYINDGDKPKVOVSYKGETKAFYPEIS 120  
 DB 61 LNPONTVFADKRLIGRKGDPVVOQSDMKHMPFOYINDGDKPKVOVSYKGETKAFYPEIS 120  
 QY 121 SMVLTKKKEIAEAYLGVPTNNAVITVPAYFNDROKATKAGYAGLVLRILINEPTAAA 180  
 DB 121 SMVLTKKKEIAEAYLGVPTNNAVITVPAYFNDROKATKAGYAGLVLRILINEPTAAA 180



```
QY 181 IAYGLDRTGKGERNVLLIFDLGGTFEDVSLITIDDGIFEVKATAGDTLHGDEFDNRNLVNH 240
D 181 IAYGLDRTGKGERNVLLIFDLGGTFEDVSLITIDDGIFEVKATAGDTLHGDEFDNRNLVNH 240
QY 241 FVEEFKRRKKKDIQONKRAVRLRTPACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300
D 241 FVEEFKRRKKKDIQONKRAVRLRTPACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300
QY 301 RFEEICSDLPFSTLEPVKALRDALKDQJHDLVVGSGSTRIPKVOXKLODFFNGRDLN 360
D 301 RFEEICSDLPFSTLEPVKALRDALKDQJHDLVVGSGSTRIPKVOXKLODFFNGRDLN 360
QY 361 KSINDEAVAYGAAYVQAAILMGDKSENVODLLLDVAPLSGLETFAGGVMATLIRKNSIT 420
D 361 KSINDEAVAYGAAYVQAAILMGDKSENVODLLLDVAPLSGLETFAGGVMATLIRKNSIT 420
QY 421 PTQTQITFTTYSNQPGLVIOYEGEERAMTKDNMLGRFELSGLIPPARGVQOIEVTEDI 480
D 421 PTQTQITFTTYSNQPGLVIOYEGEERAMTKDNMLGRFELSGLIPPARGVQOIEVTEDI 480
QY 481 DANGILNTATDKSTGKANKTITINDKGRLSKEEIERMVOAEKXKAEDEVQREHVSAN 540
D 481 DANGILNTATDKSTGKANKTITINDKGRLSKEEIERMVOAEKXKAEDEVQREHVSAN 540
QY 541 ALESYAFNMKSAYVEDEGLKGISEADKKKVLKDCQEVISWLDANTLAEKDEFEHKREKELE 600
D 541 ALESYAFNMKSAYVEDEGLKGISEADKKKVLKDCQEVISWLDANTLAEKDEFEHKREKELE 600
QY 601 QVCNPIISGLYOGAGGPGGFGAOGPKGSGSGPTIEVD 641
D 601 QVCNPIISGLYOGAGGPGGFGAOGPKGSGSGPTIEVD 641
```

## RESULT 4

```
S35718
dnak-type molecular chaperone hsp70 - pig
N:Alternate names: heat shock protein hsp70
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 09-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
R:Peelman, L.; Van de Weghe, A.R.; Coppieters, W.R.; Van Zeveren, A.J.; Bouquet, Y.H.
Immunogenetics 35, 286-289, 1992
A:Title: Complete nucleotide sequence of a porcine HSP70 gene.
A:Reference number: S35718; MUID:92175874; PMID:1339404
A:Accession: S35718
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-641 <PEP>
A:Cross-references: EMBL:M69100
C:Genetics:
A:Gene: hsp70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone
```

Query Match 97.5%; Score 3182; DB 2; Length 641;

Best Local Similarity 97.3%; Pred. No. 5.9e-168;

Matches 624; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

```
QY 1 MAKAAAGIDIGTYSYGVFOHGKVEITANDOGKRTTPTVYAFMDTERLIGDAKNQVA 60
D 1 MAKAAAGIDIGTYSYGVFOHGKVEITANDOGKRTTPTVYAFMDTERLIGDAKNQVA 60
QY 61 LNPONTVFDAKRLIGRKGDPVYVSDMKHMPFOVINDDGDKPRVOYSYKGETKAFYPEIS 120
D 61 LNPONTVFDAKRLIGRKGDPVYVSDMKHMPFOVINDDGDKPRVOYSYKGETKAFYPEIS 120
QY 121 SMVLTKEKEIAEALGYVTAAVITPVAYFENDSQOATKDGAGVLAGLVLRITNEPTAA 180
D 121 SMVLTKEKEIAEALGYVTAAVITPVAYFENDSQOATKDGAGVLAGLVLRITNEPTAA 180
QY 181 IAYGLDRTGKGERNVLLIFDLGGTFEDVSLITIDDGIFEVKATAGDTLHGDEFDNRNLVNH 240
```

```
D 181 IAYGLDRTGKGERNVLLIFDLGGTFEDVSLITIDDGIFEVKATAGDTLHGDEFDNRNLVNH 240
QY 241 FVEEFKRRKKKDIQONKRAVRLRTPACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300
D 241 FVEEFKRRKKKDIQONKRAVRLRTPACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300
QY 301 RFEEICSDLPFSTLEPVKALRDALKDQJHDLVVGSGSTRIPKVOXKLODFFNGRDLN 360
D 301 RFEEICSDLPFSTLEPVKALRDALKDQJHDLVVGSGSTRIPKVOXKLODFFNGRDLN 360
QY 361 KSINDEAVAYGAAYVQAAILMGDKSENVODLLLDVAPLSGLETFAGGVMATLIRKNSIT 420
D 361 KSINDEAVAYGAAYVQAAILMGDKSENVODLLLDVAPLSGLETFAGGVMATLIRKNSIT 420
QY 421 PTQTQITFTTYSNQPGLVIOYEGEERAMTKDNMLGRFELSGLIPPARGVQOIEVTEDI 480
D 421 PTQTQITFTTYSNQPGLVIOYEGEERAMTKDNMLGRFELSGLIPPARGVQOIEVTEDI 480
QY 481 DANGILNTATDKSTGKANKTITINDKGRLSKEEIERMVOAEKXKAEDEVQREHVSAN 540
D 481 DANGILNTATDKSTGKANKTITINDKGRLSKEEIERMVOAEKXKAEDEVQREHVSAN 540
QY 541 ALESYAFNMKSAYVEDEGLKGISEADKKKVLKDCQEVISWLDANTLAEKDEFEHKREKELE 600
D 541 ALESYAFNMKSAYVEDEGLKGISEADKKKVLKDCQEVISWLDANTLAEKDEFEHKREKELE 600
QY 601 QVCNPIISGLYOGAGGPGGFGAOGPKGSGSGPTIEVD 641
D 601 QVCNPIISGLYOGAGGPGGFGAOGPKGSGSGPTIEVD 641
```

## RESULT 5

```
I54342
dnak-type molecular chaperone HSP70 - rat
N:Alternate names: dnak-type molecular chaperone HSP70b; heat shock protein 70
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Dec-2000
C:Accession: I54342; I68986; S43388; S47522; I56574; S35955; S38199; S41413; S41414
R:Walter, L.; Kaul, F.; Gunther, E.
Immunogenetics 40, 325-330, 1994
A:Title: Comparative analysis of the three major histocompatibility complex-linked he
A:Reference number: I54342; MUID:95012453; PMID:7927536
A:Accession: I54342
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-641 <MAL2>
A:Cross-references: EMBL:X77207; NID:q1814000; PIDN:CAA54422.1; PID:9450930
A:Experimental source: HSP70.1
C:Genetics: HSP1
A:Accession: I68986
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-641 <MAL2>
A:Cross-references: EMBL:X77208; NID:9927512; PIDN:CAA54423.1; PID:9450932
A:Experimental source: HSP70.2
C:Genetics: HSP2
R:Meistril, R.; Chi, S.H.; Sayen, M.R.; Dillmann, W.H.
Biochem. J. 298, 561-569, 1994
A:Title: Isolation of a novel inducible rat heat-shock protein (HSP70) gene and its e
A:Reference number: S43388; MUID:94190258; PMID:8141767
A:Accession: S43388
A:Molecule type: DNA
A:Residues: 1-70, 'NG', '73-109', 'K', '111-203', 'R', '205-261', 'P', '263', 'ADGV', '268-641 <MESS>
A:Cross-references: EMBL:X75357; NID:9407163; PIDN:CAA53140.1; PID:9407164
A:Experimental source: ischaemic rat heart
R:Lisowska, K.; Miodak, W.; Krawczyk, Z.; Wolniczka, P.; Wisniewski, J.
Biochim. Biophys. Acta 1219, 64-72, 1994
A:Title: Cloning, nucleotide sequence and expression of rat heat inducible hsp70 gene
A:Reference number: S47522; MUID:94368874; PMID:8086479
A:Accession: S47522
A:Molecule type: DNA
A:Residues: 1-70, 'NG', '73-407', 'A', '409-641 <LIS>
```

A:Cross-references: EMBL:X74271; NID:g3413498; PIDN:CAA52328.1; PID:g396270  
A:Note: the authors translated the codon CCG for residue 365 as Asp  
R:Longo, F.M.; Wang, S.; Narasimhan, P.; Zhang, J.S.; Chen, J.; Massa, S.M.; Sharp, F.R.  
J. Neurosci. Res. 36, 325-335, 1993  
A:Title: cDNA cloning and expression of stress-induced rat hsp70 in normal and injured  
A:Reference number: 156574; MUID:94096443; PMID:8271311  
A:Accession: 156574  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-226, 'D', 228-641 <LON>  
A:Cross-references: GB:116764; NID:g294567; PIDN:AA17441.1; PID:g294568  
C:Genetics: <HSP2>  
A:Gene: hsp70.1  
C:Genetics: <HSP2>  
A:Gene: hsp70.2  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 97.1%; Score 3169; DB 2; Length 641;  
Best Local Similarity 96.6%; Pred. No. 3.1e-167;  
Matches 619; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAKAAAGIDGTTSCVGVFOHGVKEIIANDQGNRTTPSYAFDTERLIGDAKNOVA 60  
DB 1 MAKTAIGIDLTSTYSCVGVFOHGVKEIIANDQGNRTTPSYAFDTERLIGDAKNOVA 60  
QY 61 LNPQNTVFDAKRLIGRKEGDPVQSDMKHMPQVINDGDKPRVQVSYKGETAFPEETS 120  
DB 61 LNPQNTVFDAKRLIGRKEGDPVQSDMKHMPQVINDGDKPRVQVSYKGETAFPEETS 120  
QY 121 SMVLTFRKMEIAEAYIGYPYTNNAVITVPAYFNDQSQRATDAGVIAGLNTLRINEPTAA 180  
DB 121 SMVLTFRKMEIAEAYIGYPYTNNAVITVPAYFNDQSQRATDAGVIAGLNTLRINEPTAA 180  
QY 181 IAYGLDRGKGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEGDFNVLNH 240  
DB 181 IAYGLDRGKGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEGDFNVLNH 240  
QY 241 FVEEFKRHKHKKDISQNKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300  
DB 241 FVEEFKRHKHKKDISQNKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300  
QY 301 REBELCSDLFRSTLPEVEKALRDAKIDKAOIHDLVVGSTRIIPKQKLLDPEFNRLDN 360  
DB 301 REBELCSDLFRSTLPEVEKALRDAKIDKAOIHDLVVGSTRIIPKQKLLDPEFNRLDN 360  
QY 361 KSINPDEAAYGAAYOAAIILMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420  
DB 361 KSINPDEAAYGAAYOAAIILMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420  
QY 421 PTKQTOIFFTTYSNNOGVLIQVYEGERAMTKDNLLIGRELGIIPAPRGVPOIEVTFDI 480  
DB 421 PTKQTOIFFTTYSNNOGVLIQVYEGERAMTKDNLLIGRELGIIPAPRGVPOIEVTFDI 480  
QY 481 DANGILNVTATDKSTGKANKITITNDGRSLKEIERMVOEAKRYAEDEVQERYSAN 540  
DB 481 DANGILNVTATDKSTGKANKITITNDGRSLKEIERMVOEAKRYAEDEVQERYSAN 540  
QY 541 ALESTYAFNMKSAVEDGLKGISEADKKVLDKQCEVYSWLDANTLAEDKDFHKKRELE 600  
DB 541 ALESTYAFNMKSAVEDGLKGISEADKKVLDKQCEVYSWLDANTLAEDKDFHKKRELE 600  
QY 601 QVCNPIISGLYOGAGPGPGFGAGGPKGGSGGPTIEVD 641  
DB 601 QVCNPIISGLYOGAGPGPGFGAGGPKGGSGGPTIEVD 641

RESULT 6  
S31766  
dhak-type molecular chaperone hsp70 - green monkey  
N:Alternate names: heat shock protein 70

C:Species: Cercopithecus aethiops (green monkey, grivet)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S31766; 136927  
R:Salnis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
R:Salnis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
Submitted to the EMBL Data Library, January 1993  
A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock prot  
A:Reference number: 136927; MUID:95080396; PMID:7988690  
A:Accession: S31766  
A:Molecule type: mRNA  
A:Residues: 1-638 <SAI>  
R:Salnis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
FEBS Lett. 355, 282-286, 1994  
A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible  
A:Reference number: 136927; MUID:95080396; PMID:7988690  
A:Accession: 136927  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-638 <RES>  
A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
A:Experimental source: kidney; cell line COS-1  
C:Genetics:  
A:Gene: hsp70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 96.5%; Score 3148.5; DB 2; Length 638;  
Best Local Similarity 97.8%; Pred. No. 4.1e-166;  
Matches 627; Conservative 1; Mismatches 10; Indels 3; Gaps 3;

QY 1 MAKAAAGIDGTTSCVGVFOHGVKEIIANDQGNRTTPSYAFDTERLIGDAKNOVA 60  
DB 1 MAKAAAGIDGTTSCVGVFOHGVKEIIANDQGNRTTPSYAFDTERLIGDAKNOVA 60  
QY 61 LNPQNTVFDAKRLIGRKEGDPVQSDMKHMPQVINDGDKPRVQVSYKGETAFPEETS 120  
DB 61 LNPQNTVFDAKRLIGRKEGDPVQSDMKHMPQVINDGDKPRVQVSYKGETAFPEETS 120  
QY 121 SMVLTFRKMEIAEAYIGYPYTNNAVITVPAYFNDQSQRATDAGVIAGLNTLRINEPTAA 180  
DB 121 SMVLTFRKMEIAEAYIGYPYTNNAVITVPAYFNDQSQRATDAGVIAGLNTLRINEPT 179  
QY 181 IAYGLDRGKGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEGDFNVLNH 240  
DB 181 IAYGLDRGKGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDT-TWEDFDNVLNH 238  
QY 241 FVEEFKRHKHKKDISQNKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300  
DB 241 FVEEFKRHKHKKDISQNKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300  
QY 301 REBELCSDLFRSTLPEVEKALRDAKIDKAOIHDLVVGSTRIIPKQKLLDPEFNRLDN 360  
DB 301 REBELCSDLFRSTLPEVEKALRDAKIDKAOIHDLVVGSTRIIPKQKLLDPEFNRLDN 358  
QY 361 KSINPDEAAYGAAYOAAIILMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420  
DB 361 KSINPDEAAYGAAYOAAIILMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 418  
QY 421 PTKQTOIFFTTYSNNOGVLIQVYEGERAMTKDNLLIGRELGIIPAPRGVPOIEVTFDI 480  
DB 421 PTKQTOIFFTTYSNNOGVLIQVYEGERAMTKDNLLIGRELGIIPAPRGVPOIEVTFDI 477  
QY 481 DANGILNVTATDKSTGKANKITITNDGRSLKEIERMVOEAKRYAEDEVQERYSAN 540  
DB 481 DANGILNVTATDKSTGKANKITITNDGRSLKEIERMVOEAKRYAEDEVQERYSAN 537  
QY 541 ALESTYAFNMKSAVEDGLKGISEADKKVLDKQCEVYSWLDANTLAEDKDFHKKRELE 600  
DB 541 ALESTYAFNMKSAVEDGLKGISEADKKVLDKQCEVYSWLDANTLAEDKDFHKKRELE 597  
QY 601 QVCNPIISGLYOGAGPGPGFGAGGPKGGSGGPTIEVD 641  
DB 601 QVCNPIISGLYOGAGPGPGFGAGGPKGGSGGPTIEVD 641

Dh 598 QVCNPIISGLYOGAGGPGGFGAOGPKGSGSGPTIEVD 638

## RESULT 7

JH0095

dnak-type molecular chaperone hsp70 - mouse

N:Alternate names: heat shock protein 70

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Aug-1999

C:Accession: JH0095

R:Hunt, C.; Calderwood, S.

Gene 87, 199-204, 1990

A:Title: Characterization and sequence of a mouse hsp70 gene and its expression in mouse

A:Reference number: JH0095; MUID:90236310; PMID:2332169

A:Accession: JH0095

A:Molecule type: DNA

A:Residues: 1-642 <HUN>

A:Cross-references: GB:M35021; NID:g194022; PIDN:AAA37864.1; PID:g387211

A:Experimental source: strain AJ

C:Function: A:Description: involved in protein folding and assembling/disassembling of protein comp

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 95.8%; Score 3125.5; DB 2; Length 642; Best Local Similarity 95.2%; Pred. No. 7.8e-165; Matches 611; Conservative 20; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAKAAIGIDIGTGYSCVGFQHGKVEIIANDQGNRTTPSYAFETTERLIGDAKNQVA 60

Dh 1 MAKMTAIGIDIGTGYSCVGFQHGKVEIIANDQGNRTTPSYAFETTERLIGDAKNQVA 60

QY 61 LNPQNTVPDAKRLIGKRFDPVYQSDMKHMPFQVINDGDKPKQVYSKGEFAFYEEISS 120

Dh 61 LNPQNTVPDAKRLIGKRFDPVYQSDMKHMPFQVINDGDKPKQVYSKGEFAFYEEISS 120

QY 121 SMVLTQKKEIEAYLYGVPVNAVITVPAYFNDGKQATKADGAVTAGLVLRINEPTAA 180

Dh 121 SMVLTQKKEIEAYLYGVPVNAVITVPAYFNDGKQATKADGAVTAGLVLRINEPTAA 180

QY 121 SMVLTQKKEIEAYLYGVPVNAVITVPAYFNDGKQATKADGAVTAGLVLRINEPTAA 180

Dh 121 SMVLTQKKEIEAYLYGVPVNAVITVPAYFNDGKQATKADGAVTAGLVLRINEPTAA 180

QY 181 IAYGLDRTGKERNVLLFDLGGTFPDVSLITDDGIFEVKATAGDTHLGGEDFNRLVNH 240

Dh 181 IAYGLDRTGKERNVLLFDLGGTFPDVSLITDDGIFEVKATAGDTHLGGEDFNRLVNH 240

QY 241 FVEEKKRKHKKDISQNKRAVRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300

Dh 241 FVEEKKRKHKKDISQNKRAVRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300

QY 301 RFEELCSDFRSTLEPVEKALRDALDKAQLHDLVVGSTRIPKVOQLLDDFNGRDLN 360

Dh 301 RFEELCSDFRSTLEPVEKALRDALDKAQLHDLVVGSTRIPKVOQLLDDFNGRDLN 360

QY 361 KSINPEAVAYGAAYQAAIILMGDKSENVQDILLDVAPLSLGLETAGCVMTALIKRNSTI 420

Dh 361 KSINPEAVAYGAAYQAAIILMGDKSENVQDILLDVAPLSLGLETAGCVMTALIKRNSTI 420

QY 421 PKQTOIFFTYSDNPGVLIQVYEGERAMTKDNLLGFEISGLIPAPRGVPOIEVTVDI 480

Dh 421 PKQTOIFFTYSDNPGVLIQVYEGERAMTKDNLLGFEISGLIPAPRGVPOIEVTVDI 480

QY 481 DANGILNATATDKSTGKANKITITNDKGRSLSKEEIERMVOEAKYKADEVOREVSAKN 540

Dh 481 DANGILNATATDKSTGKANKITITNDKGRSLSKEEIERMVOEAKYKADEVOREVSAKN 540

QY 541 ALESYAFNMKSAVDEGLKGISEADKKRYLDKCOEIVISMLDANTLAERDEFEHKKKELE 600

Dh 541 ALESYAFNMKSAVDEGLKGISEADKKRYLDKCOEIVISMLDANTLAERDEFEHKKKELE 600

QY 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 601 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

## RESULT 8

B45871

dnak-type molecular chaperone HSP70-Hom - human

N:Alternate names: heat shock protein HSP70-Hom

C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 20-Aug-1999

C:Accession: B45871

R:Milner, C.M.; Campbell, R.D.

Immunogenetics 32, 242-251, 1990

A:Title: Structure and expression of the three MHC-1-linked HSP70 genes.

A:Reference number: A45871; MUID:91055806; PMID:1700760

A:Accession: B45871

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-641 <MLI>

A:Cross-references: GB:M59829; GB:M34268; NID:g188491; PIDN:AAA63228.1; PID:g188492

C:Function: A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 89.5%; Score 2921; DB 2; Length 641; Best Local Similarity 88.3%; Pred. No. 1.5e-153; Matches 571; Conservative 34; Mismatches 26; Indels 16; Gaps 2;

QY 2 AKAAIGIDIGTGYSCVGFQHGKVEIIANDQGNRTTPSYAFETTERLIGDAKNQVA 61

Dh 4 AKGIAIGIDIGTGYSCVGFQHGKVEIIANDQGNRTTPSYAFETTERLIGDAKNQVA 63

QY 62 NPQNTVPDAKRLIGKRFDPVYQSDMKHMPFQVINDGDKPKQVYSKGEFAFYEEISS 121

Dh 64 NPQNTVPDAKRLIGKRFDPVYQSDMKHMPFQVINDGDKPKQVYSKGEFAFYEEISS 123

QY 122 NVLTQKKEIEAYLYGVPVNAVITVPAYFNDGKQATKADGAVTAGLVLRINEPTAAI 181

Dh 124 NVLTQKKEIEAYLYGVPVNAVITVPAYFNDGKQATKADGAVTAGLVLRINEPTAAI 183

QY 182 AYGLDRTGKERNVLLFDLGGTFPDVSLITDDGIFEVKATAGDTHLGGEDFNRLVNH 241

Dh 184 AYGLDRTGKERNVLLFDLGGTFPDVSLITDDGIFEVKATAGDTHLGGEDFNRLVNH 243

QY 242 VEEFKRKHKKDISQNKRAVRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 301

Dh 244 VEEFKRKHKKDISQNKRAVRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 303

QY 302 FEEELCSDFRSTLEPVEKALRDALDKAQLHDLVVGSTRIPKVOQLLDDFNGRDLN 361

Dh 304 FEEELCSDFRSTLEPVEKALRDALDKAQLHDLVVGSTRIPKVOQLLDDFNGRDLN 363

QY 362 SINPEAVAYGAAYQAAIILMGDKSENVQDILLDVAPLSLGLETAGCVMTALIKRNSTI 421

Dh 364 SINPEAVAYGAAYQAAIILMGDKSENVQDILLDVAPLSLGLETAGCVMTALIKRNSTI 423

QY 422 PKQTOIFFTYSDNPGVLIQVYEGERAMTKDNLLGFEISGLIPAPRGVPOIEVTVDI 481

Dh 424 PKQTOIFFTYSDNPGVLIQVYEGERAMTKDNLLGFEISGLIPAPRGVPOIEVTVDI 483

QY 482 ANGLILNATATDKSTGKANKITITNDKGRSLSKEEIERMVOEAKYKADEVOREVSAKN 541

Dh 484 ANGLILNATATDKSTGKANKITITNDKGRSLSKEEIERMVOEAKYKADEVOREVSAKN 543

QY 542 LESYAFNMKSAVDEGLKGISEADKKRYLDKCOEIVISMLDANTLAERDEFEHKKKELE 601

Dh 544 LESYAFNMKSAVDEGLKGISEADKKRYLDKCOEIVISMLDANTLAERDEFEHKKKELE 603

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

Dh 604 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

QY 602 QVCNPIISGLYOGAGGPGGFGAOG- PKGSGSGPTIEVD 641

N:Alternate names: heat shock protein 70  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
C:Accession: I49761  
R:Snook, M.; Olsvsen, M.G.; van Vugt, H.; Milner, C.M.; Teuscher, C.; Campbell, R.D.  
Immunogenetics 40, 159-162, 1994  
A:Title: Coding sequences and levels of expression of Hsc70t are identical in mice with  
A:Reference number: I49761; MUID:94299288; PMID:8026864  
A:Accession: I49761  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-641 <RES>  
A:Cross-references: GB:I27086; NID:9457299; PIDN:AAA59362.1; PID:9457300  
C:Genetics:  
A:Gene: Hsc70t  
C:Function:  
A:Description: Involved in protein folding and assembling/disassembling of protein comp  
A:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 88.7%; Score 2894; DB 2; Length 641;  
Best Local Similarity 89.2%; Pred. No. 4.5e-152;  
Matches 570; Conservative 32; Mismatches 35; Indels 2; Gaps 2;

QY 3 KAAAGIDGTTTSCVGFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNQVALN 62  
DB 5 KGAATGIDGTTTSCVGFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNQVALN 64  
QY 63 PONTVDARLIRKFGDPVYOSDMKHPPOVINDGDKRVVSYGKTAFFPEISSM 122  
DB 65 PONTVDARLIRKFGDPVYOSDMKHPPOVINEAGKRVVSYGKTAFFPEISSM 124  
QY 123 VLFKMEIAEAYGYVTNAVITVPAYFNDSOQATKDGAVIAGLVNLRINEPTAAIA 182  
DB 125 VLFKMEIAEAYGYVTNAVITVPAYFNDSOQATKDGAVIAGLVNLRINEPTAAIA 184  
QY 183 YGLDRTGKGERNYLIFDLGGTFDVSILITDGIFFVKATAGDTHLGEDFDRNLVNHV 242  
DB 185 YGLDRTGKGERNYLIFDLGGTFDVSILITDGIFFVKATAGDTHLGEDFDRNLVNHV 244  
QY 243 EEFKRRHKDIISONKRAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYSTRARF 302  
DB 245 EEFKRRHKDIISONKRAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYSTRARF 304  
QY 303 EEFCSDFRSTLEPVEKALRDALDKAOIHDLVVGSTRIPVOKLLODFNGRDLNKS 362  
DB 305 EELCADLFRSTLEPVEKSLRDAMKAKIHDIYLVGSTRIPVOKLLODFNGRDLNKS 364  
QY 363 INDEAVAYGAAYVAAIILMGDKSENVODLLLDVAPLSGLETAGVMTALIKRNSTIPT 422  
DB 365 INDEAVAYGAAYVAAIILMGDKSENVODLLLDVAPLSGLETAGVMTALIKRNSTIPT 424  
QY 423 KQOQITTTSDNPGVLIQVYEEGERAMTKDNLLGRPELSGIPPARPGVQIETVDIDA 482  
DB 425 KQOQITTTSDNPGVLIQVYEEGERAMTKDNLLGRPELSGIPPARPGVQIETVDIDA 484  
QY 483 NGILNTATADKSTGKANKTTITNDKRLSKEELERVOAEKAKADEVOERESVAKNAL 542  
DB 485 NGILNTATADKSTGKANKTTITNDKRLSKEELERVOAEKAKADEVOERESVAKNAL 544  
QY 543 ESYAFNMKSAVEDEGLKGISADKKRVLDKCOEVIISMLDANTLAEDFEHRRKELEOV 602  
DB 545 ESYAFNMKSAVEDEGLKDKISSEDDKKIILDKCNEVLSWLEANDLAKEDFDHRRKELENN 604  
QY 603 CNPIISGLYQAGAGPGGFGAAGPKGSGSGPTIEVD 641  
DB 605 CNPIITKLYQ-SGCTGPTCTPGYTP-GRATGPTIEVD 641

RESULT 10  
S41415  
dnak-type molecular chaperone Hsp70.3 - rat  
N:Alternate names: heat shock protein 70

C:Species: Rattus norvegicus (Norway rat)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jul-2000  
C:Accession: S41415; I68987  
R:Ruitz, W.  
submitted to the EMBL Data Library, January 1994  
A:Reference number: S41415  
A:Accession: S41415  
A:Molecule type: DNA  
A:Residues: 1-641 <LUT>  
A:Cross-references: EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:9450934  
R:Walter, L.; Raun, F.; Gunther, E.  
Immunogenetics 40, 325-330, 1994  
A:Title: Comparative analysis of the three major histocompatibility complex-linked he  
A:Reference number: I54542; MUID:95012453; PMID:7927536  
A:Accession: I68987  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-641 <RES>  
A:Cross-references: EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:9450934  
C:Genetics:  
A:Gene: Hsp70-3  
C:Function:  
A:Description: Involved in protein folding and assembling/disassembling of protein co  
A:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 88.3%; Score 2882; DB 2; Length 641;  
Best Local Similarity 88.6%; Pred. No. 2.1e-151;  
Matches 569; Conservative 32; Mismatches 33; Indels 8; Gaps 3;

QY 3 KAAAGIDGTTTSCVGFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNQVALN 62  
DB 5 KGAATGIDGTTTSCVGFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNQVALN 64  
QY 63 PONTVDARLIRKFGDPVYOSDMKHPPOVINDGDKRVVSYGKTAFFPEISSM 122  
DB 65 PONTVDARLIRKFGDPVYOSDMKHPPOVINEAGKRVVSYGKTAFFPEISSM 124  
QY 123 VLFKMEIAEAYGYVTNAVITVPAYFNDSOQATKDGAVIAGLVNLRINEPTAAIA 182  
DB 125 VLFKMEIAEAYGYVTNAVITVPAYFNDSOQATKDGAVIAGLVNLRINEPTAAIA 184  
QY 183 YGLDRTGKGERNYLIFDLGGTFDVSILITDGIFFVKATAGDTHLGEDFDRNLVNHV 242  
DB 185 YGLDRTGKGERNYLIFDLGGTFDVSILITDGIFFVKATAGDTHLGEDFDRNLVNHV 244  
QY 243 EEFKRRHKDIISONKRAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYSTRARF 302  
DB 245 EEFKRRHKDIISONKRAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYSTRARF 304  
QY 303 EEFCSDFRSTLEPVEKALRDALDKAOIHDLVVGSTRIPVOKLLODFNGRDLNKS 362  
DB 305 EELCADLFRSTLEPVEKSLRDAMKAKIHDIYLVGSTRIPVOKLLODFNGRDLNKS 364  
QY 363 INDEAVAYGAAYVAAIILMGDKSENVODLLLDVAPLSGLETAGVMTALIKRNSTIPT 422  
DB 365 INDEAVAYGAAYVAAIILMGDKSENVODLLLDVAPLSGLETAGVMTALIKRNSTIPT 424  
QY 423 KQOQITTTSDNPGVLIQVYEEGERAMTKDNLLGRPELSGIPPARPGVQIETVDIDA 482  
DB 425 KQOQITTTSDNPGVLIQVYEEGERAMTKDNLLGRPELSGIPPARPGVQIETVDIDA 484  
QY 483 NGILNTATADKSTGKANKTTITNDKRLSKEELERVOAEKAKADEVOERESVAKNAL 542  
DB 485 NGILNTATADKSTGKANKTTITNDKRLSKEELERVOAEKAKADEVOERESVAKNAL 544  
QY 543 ESYAFNMKSAVEDEGLKGISADKKRVLDKCOEVIISMLDANTLAEDFEHRRKELEOV 602  
DB 545 ESYAFNMKSAVEDEGLKDKISSEDDKKIILDKCNEVLSWLEANDLAKEDFDHRRKELENN 604  
QY 603 CNPIISGLYQ-GAGCP--GGGFGAAGPKGSGSGPTIEVD 641  
DB 605 CNPIITKLYQ-SGCTGPTCTPGCAPG-----YTPGARANTGPTIEVD 641

## RESULT 11

dnak-type molecular chaperone hsc73 - rat  
S07197

N/Alternate names: heat shock cognate protein hsc70; heat shock cognate protein hsc73  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 20-Aug-1999

C/Accession: S07197; 157594; S35606

R/Sorger, P.K.; Pelham, H.R.B.

EMBL J. 6, 993-998, 1987

A/Title: Cloning and expression of a gene encoding hsc73, the major hsp70-like protein in A/Reference number: S07197; MUID:87246537; PMID:3595567

A/Accession: S07197

A/Molecule type: DNA

A/Residues: 1-646 <SOR>

A/Cross-references: EMBL:Y00054; NID:g56378; PIDN:CA68265.1; PID:g56379

R/O'Malley, K.; Mauron, A.; Barchas, J.D.; Kedes, L.  
Mol. Cell. Biol. 5, 3476-3483, 1985

A/Title: Constitutively expressed rat mRNA encoding a 70-kilodalton heat-shock-like prot A/Reference number: 157594; MUID:86310827; PMID:3939319

A/Accession: 157594

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-646 <RES>

A/Molecule type: mRNA

A/Cross-references: GB:M11942; NID:g204666; PIDN:AAA1354.1; PID:g204667

R/Wang, C.; Lee, M.R.

Biochem. J. 294, 69-77, 1993

A/Title: High-level expression of soluble rat hsc70 in Escherichia coli: purification an A/Reference number: S35606; MUID:93371384; PMID:8363588

A/Accession: S35606

A/Molecule type: protein

A/Residues: 2-40 <MAN>

C/Genetics: hsc73; hsc70

A/Intons: 137/3; 188/3; 374/1; 441/3; 508/1; 585/3

C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein comp

C/Superfamily: heat shock protein 70

C/Keywords: ATP; molecular chaperone

F/2-646/Product: dnak-type molecular chaperone hsc73 #status experimental <MAT>

Query Match

Best Local Similarity 87.7%; Score 2862.5; DB 2; Length 646;  
Matches 554; Conservative 47; Mismatches 40; Indels 5; Gaps 3;

QY 1 MAKAAIGIDLGTTYSVGVFQHGKVELIANDGNNRTTPSYVAFTDRLIGDAKNQVA 60  
D 1 MSKPAVIGIDLGTTYSVGVFQHGKVELIANDGNNRTTPSYVAFTDRLIGDAKNQVA 60  
QY 61 LNPONTVDKARKLIGRKFDVYVSDMKHMPVOYINDGDKRVOYSGETKATPEETS 120  
D 61 MNPNTVFDKARKLIGRKFDVYVSDMKHMPVOYINDGDKRVOYSGETKATPEETS 120  
QY 121 SMVLTKKKEIEATLYGVPVNAVTVPAYFNDSDQKATKDVAGLNLINPTPAAA 180  
D 121 SMVLTKKKEIEATLYGVPVNAVTVPAYFNDSDQKATKDVAGLNLINPTPAAA 180  
QY 181 IAYGLDRTGKERNLIFDLGGTFDVSILITIDGIEFVKATAGDTHLGSDPNNRLVNH 240  
D 181 IAYGLDRTGKERNLIFDLGGTFDVSILITIDGIEFVKATAGDTHLGSDPNNRLVNH 240  
QY 241 FVEEFKKRHKDDISQNKRAVRLRTACERAKRTLSSTQASLEIDSLEFGIDFTTSTRA 300  
D 241 FVEEFKKRHKDDISQNKRAVRLRTACERAKRTLSSTQASLEIDSLEFGIDFTTSTRA 300  
QY 301 RFEELCSDLFSTLEPEKALRDALKDAQJHDLVVGSGTRIPKVOKLDDFFNGRDLN 360  
D 301 RFEELCSDLFSTLEPEKALRDALKDAQJHDLVVGSGTRIPKVOKLDDFFNGRDLN 360  
QY 361 KSINPDEAVAGAAVQAAILMGDKSENVQDILLDLVAPLSGLETFAGVMTALIKRNSTI 420  
D 361 KSINPDEAVAGAAVQAAILMGDKSENVQDILLDLVAPLSGLETFAGVMTALIKRNSTI 420

## RESULT 12

dnak-type molecular chaperone hsc73 - mouse  
JC4853

N/Alternate names: heat-shock protein 73  
C/Species: Mus musculus (house mouse)

C/Date: 15-Aug-1996 #sequence\_revision 18-Oct-1996 #text\_change 20-Aug-1999

C/Accession: JC4853

R/Soulier, S.; Vilotte, J.L.; L'Huillier, P.J.; Mercier, J.C.

Gene 172, 285-289, 1996

A/Title: Developmental regulation of murine integrin beta1 subunit- and Hsc73-encodin A/Reference number: JC4853; MUID:96269419; PMID:8682318

A/Contents: mammary gland

A/Molecule type: mRNA

A/Residues: 1-646 <SOU>

A/Cross-references: GB:U27129; NID:g861212; PIDN:AAC52836.1; PID:g861213

A/Comment: This protein plays a role during mamogenesis and is involved in the contro

C/Genetics: hsc73

C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein co

C/Superfamily: heat shock protein 70

C/Keywords: ATP; mammary gland; molecular chaperone

Query Match

Best Local Similarity 85.8%; Score 2862.5; DB 2; Length 646;  
Matches 554; Conservative 47; Mismatches 40; Indels 5; Gaps 3;

QY 1 MAKAAIGIDLGTTYSVGVFQHGKVELIANDGNNRTTPSYVAFTDRLIGDAKNQVA 60  
D 1 MSKPAVIGIDLGTTYSVGVFQHGKVELIANDGNNRTTPSYVAFTDRLIGDAKNQVA 60  
QY 61 LNPONTVDKARKLIGRKFDVYVSDMKHMPVOYINDGDKRVOYSGETKATPEETS 120  
D 61 MNPNTVFDKARKLIGRKFDVYVSDMKHMPVOYINDGDKRVOYSGETKATPEETS 120  
QY 121 SMVLTKKKEIEATLYGVPVNAVTVPAYFNDSDQKATKDVAGLNLINPTPAAA 180  
D 121 SMVLTKKKEIEATLYGVPVNAVTVPAYFNDSDQKATKDVAGLNLINPTPAAA 180  
QY 181 IAYGLDRTGKERNLIFDLGGTFDVSILITIDGIEFVKATAGDTHLGSDPNNRLVNH 240  
D 181 IAYGLDRTGKERNLIFDLGGTFDVSILITIDGIEFVKATAGDTHLGSDPNNRLVNH 240  
QY 241 FVEEFKKRHKDDISQNKRAVRLRTACERAKRTLSSTQASLEIDSLEFGIDFTTSTRA 300  
D 241 FVEEFKKRHKDDISQNKRAVRLRTACERAKRTLSSTQASLEIDSLEFGIDFTTSTRA 300  
QY 301 RFEELCSDLFSTLEPEKALRDALKDAQJHDLVVGSGTRIPKVOKLDDFFNGRDLN 360  
D 301 RFEELCSDLFSTLEPEKALRDALKDAQJHDLVVGSGTRIPKVOKLDDFFNGRDLN 360  
QY 361 KSINPDEAVAGAAVQAAILMGDKSENVQDILLDLVAPLSGLETFAGVMTALIKRNSTI 420  
D 361 KSINPDEAVAGAAVQAAILMGDKSENVQDILLDLVAPLSGLETFAGVMTALIKRNSTI 420

QY	421	PKKQOITFTTYS	DNQGV	LIOY	EBE	RAMTKDN	NLL	SP	ELSG	IP	PAR	GO	LE	VED	I	480
Db	421	PKKQOITFTTYS	DNQGV	LIOY	EBE	RAMTKDN	NLL	SP	ELSG	IP	PAR	GO	LE	VED	I	480
QY	481	DANGILNANTAT	DSTG	KANK	ITIT	NTDK	GR	LSKE	IE	IR	VO	EA	EK	YKA	DE	540
Db	481	DANGILNANTAT	DSTG	KANK	ITIT	NTDK	GR	LSKE	IE	IR	VO	EA	EK	YKA	DE	540
QY	541	ALIESAFNMK	SAVED	EG	LK	GTISE	AD	KK	VLD	KCO	EV	I	SW	L	DANT	600
Db	541	ALIESAFNMK	SAVED	EG	LK	GTISE	AD	KK	VLD	KCO	EV	I	SW	L	DANT	600
QY	601	OVCNFIITSL	GYOG	AGG	-PG	G	-	GA	OG	PK	GS	GS	G	P	TE	641
Db	601	OVCNFIITSL	GYOG	AGG	-PG	G	-	GA	OG	PK	GS	GS	G	P	TE	641

```

RESULT 13
A:27077
N:dnak-type molecular chaperone - human
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 13-Mar-1998
C:Accession: A27077
R:R.Dworniczak, B.; Mirault, M.E.
Nucleic Acids Res. 15, 5181-5197, 1987
A:Title: Structure and expression of a human gene coding for a 71 kd heat shock 'cognate'
A:Reference number: A27077; MUID:87255994; PMID:3037489
A:Accession: A27077
A:Molecule type: DNA
A:Residues: 1-646 <DMC>
A:Cross-references: GH:M19141
C:Genetics:
A:Introns: 69/1; 137/3; 188/3; 374/1; 441/3; 508/1; 585/3
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

```

Query Match	87.6%	Score 2859.5	DB 2	Length 646
Best Local Similarity	85.6%	Pred. No. 3.6e-150		
Matches	553	Conservative 48	Mismatches 40	Indels 5
				Gaps 3
QY	1	MAKAAAGIDGGTTCVGVFOHKGVELIANDQGNRTTSPYAFETDRLIGDAKNOVA	60	
		1	MSKPAVAGIDGGTTCVGVFOHKGVELIANDQGNRTTSPYAFETDRLIGDAKNOVA	60
QY	61	LNPOPTVDARKLIGRKGKGDVPYOSDMKHMPROVINDDCKRKYQVSYGKFAKPEEIS	120	
	61	KMPITVTVDARKLIGRKGKGDVPYOSDMKHMPROVINDDCKRKYQVSYGKFAKPEEIS	120	
QY	121	SMVLTAKMEIEAVALGYEPTNAVITVPAYFENDSQOATKDGAVIGLVLRINEPTAAA	180	
	121	SMVLTAKMEIEAVALGYEPTNAVITVPAYFENDSQOATKDGAVIGLVLRINEPTAAA	180	
QY	181	IAYGDRKGKGRNVLIDGGGTFDVSILITDQIEFVAKTAGTHLGGDFDNRLYNH	240	
	181	IAYGDRKGKGRNVLIDGGGTFDVSILITDQIEFVAKTAGTHLGGDFDNRLYNH	240	
QY	241	FVEEKKRKHKKDISONKRAVRLRTPACERAKRTLSSSTQASLETIDSLGEGIDFYISITRA	300	
	241	FVEEKKRKHKKDISONKRAVRLRTPACERAKRTLSSSTQASLETIDSLGEGIDFYISITRA	300	
QY	301	RFEELCSLFFSTLEPVRKALRDAKLDKAQIHDVLVCGSTRIRPVOKLLDDFFRGRDLN	360	
	301	RFEELCSLFFSTLEPVRKALRDAKLDKAQIHDVLVCGSTRIRPVOKLLDDFFRGRDLN	360	
QY	361	KSINDEKVAAGAAVQAAILMGDKSENVQDILLDVAFLSGLETAGVAMTALIKRNTTI	420	
	361	KSINDEKVAAGAAVQAAILMGDKSENVQDILLDVAFLSGLETAGVAMTALIKRNTTI	420	
QY	421	PTKQTQITFTTYSNDOPCVLIOYBESERAMTKDNNLLGFEELSGIIPADRGVQPIEVTFDI	480	

```

Db 421 PTKOTQTFPTTYSNDQPGVLIQVYEGEAMTKDNNNLCKFELTETIPAPPGVQPIEVTEPI 480
      |||
Qy 481 DANGILNVTATDKSTGKANKTITINDGRLSKEIEIEMVOEAKRYAEDEVOREYRSAXN 540
      |||
Db 481 DANGILNVSANDKSTGKANKTITINDGRLSKEDIEMVOEAKRYAEDEKQORDKXSSN 540
      |||
Qy 541 ALESAEYAFNMKSAVEDEGLCKITSEADKKVLDCQEVISWLDANTLAEKDEFEHKELE 600
      |||
Db 541 SLESAEYAFNMKTYVEDEKLOCKINDEKOKILDCNELLINMLDNQJAEKEBEFEHCKELE 600
      |||
Qy 601 QVCNPDIISGLYQAGG--PGG--GAQPGKGGSGSGPTIEYD 641
      |||
Db 601 KVCNPDIITKLQYAGSGMPGCGMPGCFPGGAGAPPSGGASGPTIEYD 646
      |||

```

RESULT 14  
S31716  
dnak-type molecular chaperone hsp72-ps1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jan-1995 #sequence\_rev13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: 160329; S31716  
R:Walter, L.; Helne, L.; Gunther, E.  
I:Immunogenetics 39, 351-354, 1994  
A:Title: Sequence, expression, and mapping of a rat Mhc class Ib gene.  
A:Reference number: 160329; PMID:7545923  
A:Accession: 160329  
A:Status: preliminary; translated from GR/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-646 (#R35)  
A:Cross-references: EMBL:X70065; NID:956384; PIDN:CAA49670.1; PID:956385  
C:Genetics:  
A:Gene: hsp72-ps1  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

[illegible]



**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen, Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:47:43 ; Search time 14 Seconds  
(without alignments)  
1899.023 Million cell updates/sec

Title: US-09-646-835-1  
Perfect score: 641  
Sequence: 1 MAKAAATGIDIGTTCVGV.....FGAGPKGSGSGPTIEVD 641

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwisProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	641	100.0	641	1 HS71_HUMAN	P08107 homo sapien
2	370	57.7	641	1 HS71_BOVIN	Q27975 bos taurus
3	370	57.7	641	1 HS72_BOVIN	Q27965 bos taurus
4	209	32.6	641	1 HS71_PIG	P34930 sus scrofa
5	175	27.3	638	1 HS71_CERAE	Q28222 cercopithec
6	114	17.8	641	1 HS71_RAT	Q07439 rattus norv
7	101	15.8	641	1 HS71_MOUSE	P17879 mus musculu
8	80	12.5	420	1 HS73_MOUSE	Q61696 mus musculu
9	57	8.9	639	1 HS71_ORYLA	Q918f9 oryzias lat
10	55	8.6	633	1 HS72_MOUSE	P17156 mus musculu
11	55	8.6	633	1 HS72_RAT	P16659 rattus norv
12	55	8.6	634	1 HS70_CHICK	P08106 gallus gall
13	55	8.6	639	1 HS72_HUMAN	P54652 homo sapien
14	55	8.6	641	1 HS73_RAT	P55063 rattus norv
15	55	8.6	641	1 HS7H_HUMAN	P14931 homo sapien
16	55	8.6	641	1 HS7T_MOUSE	P16627 mus musculu
17	54	8.4	644	1 HS70_ONCTS	Q91233 oncorhynch
18	53	8.3	646	1 HS7C_CRIGR	P13738 cricetus
19	53	8.3	646	1 HS7C_HUMAN	P08109 mus musculu
20	53	8.3	646	1 HS7C_MOUSE	P08109 mus musculu
21	53	8.3	647	1 HS70_XENLA	P02872 xenopus lae
22	53	8.3	649	1 HS7C_BRARE	Q09473 brachydanio
23	53	8.3	650	1 HS7C_BOVIN	P11120 bos taurus
24	53	8.3	651	1 HS7D_DROME	P11147 drosophila
25	53	8.3	686	1 HS7C_ORYLA	Q946y1 oryzias lat
26	50	7.8	372	1 HS72_PARLI	P26623 paracrot
27	47	7.3	631	1 HS73_BOVIN	P34933 bos taurus
28	47	7.3	643	1 HS76_HUMAN	P17066 homo sapien
29	44	6.9	654	1 HS70_HYDMA	Q05944 hydra magni
30	43	6.7	645	1 HS70_PLEWA	Q91291 pleurodeles
31	42	6.6	379	1 HS7X_PIG	P34934 sus scrofa
32	42	6.6	643	1 HS76_PIG	Q04967 sus scrofa
33	42	6.6	653	1 HS72_ARATH	P22954 arabidopsis

34	41	6.4	637	1 HS70_SCHMA	P08418 schistosoma
35	40	6.2	652	1 HS7D_MANSE	Q94639 manduca sex
36	39	6.1	640	1 HS71_ANOAL	P41825 anopheles a
37	39	6.1	640	1 HS72_ANOAL	P41826 anopheles a
38	39	6.1	640	1 HS74_ANOAL	P41827 anopheles a
39	39	6.1	649	1 HS7C_ICRPU	P47773 ictalurus p
40	39	6.1	651	1 HS70_ONCMY	P08108 oncorhynch
41	38	5.9	214	1 HS7A_DROSI	P02826 drosophila
42	38	5.9	640	1 HS7A_CAEEL	P03446 caenorhabdi
43	38	5.9	641	1 HS7A_DROME	P23843 drosophila
44	38	5.9	644	1 HS70_BRUMA	P27541 brugia mala
45	35	5.5	640	1 HS7C_DICDI	P36415 dictyosteli

## ALIGNMENTS

RESULT 1  
ID HS71\_HUMAN STANDARD: PRT: 641 AA.  
AC P08107: P19790; Q9UQMO; Q9UQL9;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).  
CN (HSPA1A OR HSPA1) AND HSPA1B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP  
RX MEDLINE-91055806; PubMed-1700760;  
RA Milner C.M., Campbell R.D.;  
RT "Structure and expression of the three MHC-linked HSP70 genes.";  
RL Immunogenetics 32:242-251(1990).  
RN [2]  
RP  
RX SEQUENCE FROM N.A.  
RA MEDLINE-86016721; PubMed-3931075;  
RA Hunt C., Morimoto R.I.;  
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison  
with the nucleotide sequence of human hsp70.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).  
RN [3]  
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).  
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,  
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Young J.,  
RA Laskey S., Hood L.;  
RT "Sequence of the human major histocompatibility complex class III  
region.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).  
RA Shina S., Tamiya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.  
RA MEDLINE-89184548; PubMed-2538825;  
RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;  
RT "Human major histocompatibility complex contains genes for the major  
heat shock protein HSP70.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).  
RN [6]  
RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.  
RA MEDLINE-87066768; PubMed-3786141;  
RA Drabent B., Genthe A., Benecke B.-J.;  
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts  
prepared from heat-shocked and non-heat-shocked human cells.";  
RL Nucleic Acids Res. 14:8933-8949(1986).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.  
RA MEDLINE-99234376; PubMed-10216320;

RA Osipuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;  
 RT "Structure of a new crystal form of human hsp70 ATPase domain.";  
 RL Acta Crystallogr. D 55:1105-1107(1999).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
 CC PROTEIN TRANSDUCTION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
 CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
 CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
 CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXPOSED PEPTIDE  
 CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
 CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
 CC STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M59828; AAA63226.1; -;  
 DR EMBL: M59830; AAA63227.1; -;  
 DR EMBL: AF134726; AAD21816.1; -;  
 DR EMBL: AF134726; AAD21816.1; -;  
 DR EMBL: AP000503; BAB63300.1; -;  
 DR EMBL: AP000503; BAB63299.1; -;  
 DR EMBL: M11717; AAA52697.1; -;  
 DR EMBL: M24743; AAA59844.1; -;  
 DR EMBL: M24744; AAA59845.1; -;  
 DR EMBL: X04676; CAA28381.1; -;  
 DR EMBL: X04677; CAA28382.1; -;  
 DR PIR: A29160; A29160.  
 DR PIR: A45871; A45871.  
 DR PIR: A25773; A25773.  
 DR PDB: 1HU0; 21-OCT-98.  
 DR SWISS-2DPAGE: P08107; HUMAN.  
 DR Genew: HGNC:5232; HSPA1A.  
 DR Genew: HGNC:5233; HSPA1B.  
 DR MIM: 140550; -;  
 DR MIM: 603012; -;  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PRODOM: PD000089; HSP70; 1.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW ATP-binding; Chaperone; Heat shock; Multigene family;  
 KW 3D-structure.  
 FT CONFLICT 7 7 I -> V (IN REF. 2).  
 FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).  
 FT CONFLICT 370 370 A -> G (IN REF. 2).  
 FT CONFLICT 469 469 MISSING (IN REF. 2).  
 FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).  
 SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96DE6 CRC64;  
 Query Match 100.0%; Score 641; DB 1; Length 641;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 SMVLTKKKEIAEAYIGPYTNAVITVPAYFNDSORATKAGVLAGLVRLINEPTAA 180  
 DB 121 SMVLTKKKEIAEAYIGPYTNAVITVPAYFNDSORATKAGVLAGLVRLINEPTAA 180  
 QY 181 IAVGLDRTGGERNVLLIFDLGGTFDVSILITIDGIFEVKATAGDTHLGGEDFNRLVNH 240  
 DB 181 IAVGLDRTGGERNVLLIFDLGGTFDVSILITIDGIFEVKATAGDTHLGGEDFNRLVNH 240  
 QY 241 FVEEFKKKKKDISQNKRAVRRLTAECERAKRTLSSTQASLEIDSIFEGTIDETSTRA 300  
 DB 241 FVEEFKKKKKDISQNKRAVRRLTAECERAKRTLSSTQASLEIDSIFEGTIDETSTRA 300  
 QY 241 FVEEFKKKKKDISQNKRAVRRLTAECERAKRTLSSTQASLEIDSIFEGTIDETSTRA 300  
 DB 241 FVEEFKKKKKDISQNKRAVRRLTAECERAKRTLSSTQASLEIDSIFEGTIDETSTRA 300  
 QY 301 RFEELCSDLRSTLEPEKALRDAKDKAOIHDLVVGSGSTRIPKVKLLDGFNGHDLN 360  
 DB 301 RFEELCSDLRSTLEPEKALRDAKDKAOIHDLVVGSGSTRIPKVKLLDGFNGHDLN 360  
 QY 361 KSINPDEAVAYGAAYQAAILMGKSENVODLLLDVAPLSLGLETAGVMTALIKRNSTI 420  
 DB 361 KSINPDEAVAYGAAYQAAILMGKSENVODLLLDVAPLSLGLETAGVMTALIKRNSTI 420  
 QY 421 PTXOTQLETTYSDNQPGVLLQVYEGERAMTKDNNLGRFELSGIPPAKGVPOIEVFDI 480  
 DB 421 PTXOTQLETTYSDNQPGVLLQVYEGERAMTKDNNLGRFELSGIPPAKGVPOIEVFDI 480  
 QY 481 DANGLVNTATDKSTGKANKITTYNDKGRLSKEIEHMOEAERYKADEVOERVSANK 540  
 DB 481 DANGLVNTATDKSTGKANKITTYNDKGRLSKEIEHMOEAERYKADEVOERVSANK 540  
 QY 541 ALESYAFNMKSAVEDGLKGRKISEADKKRYVLDKQCEVISMUDANTLAEKDEPEHKKKELE 600  
 DB 541 ALESYAFNMKSAVEDGLKGRKISEADKKRYVLDKQCEVISMUDANTLAEKDEPEHKKKELE 600  
 QY 601 QVCNPITISGLYQAGGPGGPGGAGQGPGRGSGGSGPTIEVD 641  
 DB 601 QVCNPITISGLYQAGGPGGPGGAGQGPGRGSGGSGPTIEVD 641  
 RESULT 2  
 HS71\_BOVIN STANDARD; PRT; 641 AA.  
 ID HS71\_BOVIN  
 AC Q27975; Q27964;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Heat shock 70 kDa protein 1 (HSP70-1).  
 GN HSP70-1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=95126904; PubMed=7826329;  
 RA Gutierrez J.A., Guerrero V.;  
 RT "Chemical modifications of a recombinant bovine stress-inducible 70  
 RT kDa heat-shock protein (hsp70) mimics Hsp70 isoforms from tissues";  
 RL Biochem. J. 305:197-203(1995).  
 RN [2]  
 RP SEQUENCE OF 212-641 FROM N.A.  
 RC STRAIN=Angus;  
 RX MEDLINE=95030563; PubMed=7943958;  
 RA Gross M.D., Skow L.C., Stone R.T.;  
 RT "An Alu1 polymorphism at the bovine 70 kD heat-shock protein-1  
 RT (HSP70-1) locus.";  
 RL Anim. Genet. 25:196-196(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR

```

CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATION OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U09861; AAA73914.1; -
DR EMBL; U02891; AAA03450.1; -
DR HSSP; P08107; IHUO.
DR InterPro: IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; HSP70_1; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
DR SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 57.7%; Score 370; DB 1; Length 641;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 PVTNAVITVPAYFNDSSQOATKRDAGVLAGLVNLRINEPTAAAIAYGIDRTGKGERNVLI 197
DB 138 PVTNAVITVPAYFNDSSQOATKRDAGVLAGLVNLRINEPTAAAIAYGIDRTGKGERNVLI 197

QY 198 FDLGGGTFDVSILITIDSGIFEVKATAGDTHLGGEFDNRRLVNHVEEKKRHKHDKDISONK 257
DB 198 FDLGGGTFDVSILITIDSGIFEVKATAGDTHLGGEFDNRRLVNHVEEKKRHKHDKDISONK 257

QY 258 RAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYSITRAREELCSOLFSTLEPV 317
DB 258 RAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYSITRAREELCSOLFSTLEPV 317

QY 318 EKALRDALKDAQIHDVLVVGSTRIPKVKOKLLODFENGRLNKSINPDEAVAYGAAYQA 377
DB 318 EKALRDALKDAQIHDVLVVGSTRIPKVKOKLLODFENGRLNKSINPDEAVAYGAAYQA 377

QY 378 AILMGDSKENVODLLLDVAPLSGLETAGCVMTALIKRNSITPTKQTQITFTYSDNPG 437
DB 378 AILMGDSKENVODLLLDVAPLSGLETAGCVMTALIKRNSITPTKQTQITFTYSDNPG 437

QY 438 VLIQVYSEERAMTDNNLIGREELSGTPPARGVQQLTEVTEDIDANGILNTATDKSTGK 497
DB 438 VLIQVYSEERAMTDNNLIGREELSGTPPARGVQQLTEVTEDIDANGILNTATDKSTGK 497

QY 498 ANKTTITNDKGRLSKEELERVAOEAKEYKADEVOERERVSANKNALESAFNNKSAVEDEG 557
DB 498 ANKTTITNDKGRLSKEELERVAOEAKEYKADEVOERERVSANKNALESAFNNKSAVEDEG 557

QY 558 LKGIISADKKKVLDKCOEVIISWLDANTLAEKDEFEHKKRELEOVCPNIIS 608
DB 558 LKGIISADKKKVLDKCOEVIISWLDANTLAEKDEFEHKKRELEOVCPNIIS 608

RESULT 3
HS72_BOVIN STANDARD; PRT; 641 AA.
AC 027965; 028122;
DT 01-NOV-1997 (Rel. 35, Created)

```

```

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DB Heat shock 70 kDa protein 2 (HSP70-2).
GN HSP70-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94070117; PubMed=8249428;
RA Kowalski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,
RA van den Hurk J., Babluk L.A., Zamb T.J.;
RT "Heat-shock promoter-driven synthesis of secreted bovine herpesvirus
RT glycoproteins in transfected cells.";
RL Vaccine 11:1100-1107(1993).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U02892; AAA03451.1; -
DR EMBL; M98823; AAA30568.1; -
DR HSSP; P08107; IHUO.
DR InterPro: IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; HSP70_1; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
DR SEQUENCE 641 AA; 70228 MW; 229C19EEB8F10DF CRC64;

Query Match 57.7%; Score 370; DB 1; Length 641;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 PVTNAVITVPAYFNDSSQOATKRDAGVLAGLVNLRINEPTAAAIAYGIDRTGKGERNVLI 197
DB 138 PVTNAVITVPAYFNDSSQOATKRDAGVLAGLVNLRINEPTAAAIAYGIDRTGKGERNVLI 197

QY 198 FDLGGGTFDVSILITIDSGIFEVKATAGDTHLGGEFDNRRLVNHVEEKKRHKHDKDISONK 257
DB 198 FDLGGGTFDVSILITIDSGIFEVKATAGDTHLGGEFDNRRLVNHVEEKKRHKHDKDISONK 257

QY 258 RAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYSITRAREELCSOLFSTLEPV 317
DB 258 RAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYSITRAREELCSOLFSTLEPV 317

```

```

Db 258 RAVRLRTACERAKRTLSSSTQASLEIDSLFEGIDFVTSITRARFELCSDLFIRSTLEPV 317
QY 318 EKALRPDAKLKAOIHDLVVGSGSTRIPKVKLLQDFFNGRDLKSNINPEAAYGAAYCA 377
Db 318 EKALRPDAKLKAOIHDLVVGSGSTRIPKVKLLQDFFNGRDLKSNINPEAAYGAAYCA 377
QY 378 AIIIMGDKSENVODLLLDVAPLSLGLTAGVMTALIKRNSTIPTKQTOIFTTYSDNQPG 437
Db 378 AIIIMGDKSENVODLLLDVAPLSLGLTAGVMTALIKRNSTIPTKQTOIFTTYSDNQPG 437
QY 438 VILQVVEGERAMTRDNNLGRFELSGIPAPRGVPOLEVFEDIDANGILNVTATDSTGK 497
Db 438 VILQVVEGERAMTRDNNLGRFELSGIPAPRGVPOLEVFEDIDANGILNVTATDSTGK 497
QY 498 ANKITTINDGRSLKEBIEERMOEAERKKADEVOERERVAKNALLESYAFNMKSAVEDG 557
Db 498 ANKITTINDGRSLKEBIEERMOEAERKKADEVOERERVAKNALLESYAFNMKSAVEDG 557
QY 558 LKGRISEADKKKVLDCQEVISWLDANTLAEKDFEHRKRELEQVCNPILIS 608
Db 558 LKGRISEADKKKVLDCQEVISWLDANTLAEKDFEHRKRELEQVCNPILIS 608

RESULT 4
HS7L_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70.1).
GN HSPAL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J., de Weyhe A.R., Coppieters W.R., van Zeveren A.J.,
RA Bouquet Y.H.;
RT "Complete nucleotide sequence of a porcine HSP70 gene.";
RL Immunogenetics 35:286-289(1992).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M69100; -; NOT_ANNOTATED_CDS.
CC PIR; S35718; S35718.
CC HSSP; P08107; 1H0.
CC Interpret; IPRO01023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PRODOM; PD000089; HSP70; 1.
CC PROSITE; PS00297; HSP70.1; 1.
CC PROSITE; PS00329; HSP70.2; 1.
CC PROSITE; PS01036; HSP70.3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
CC SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;

```

```

Query Match 32.6%; Score 209; DB 1; Length 641;
Best Local Similarity 99.7%; Pred. No. 1.3e-203;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 141 NAVITVPAYFNDSORATDAGYIAGLVRLIINEPTAAIAVAGLDRTGKERNULEFL 200
Db 141 NAVITVPAYFNDSORATDAGYIAGLVRLIINEPTAAIAVAGLDRTGKERNULEFL 200
QY 201 GGSTFVSLTIDDDIFEVKATAGDTHLGEDDNLVHFEERKRRKKDLSQNKRAV 260
Db 201 GGSTFVSLTIDDDIFEVKATAGDTHLGEDDNLVHFEERKRRKKDLSQNKRAV 260
QY 261 RRLRTACERAKRTLSSSTQASLEIDSLFEGIDFVTSITRARFELCSDLFIRSTLEPEKA 320
Db 261 RRLRTACERAKRTLSSSTQASLEIDSLFEGIDFVTSITRARFELCSDLFIRSTLEPEKA 320
QY 321 LRDAKLDAKAOIHDLVVGSGSTRIPKVKLLQDFFNGRDLKSNINPEAAYGAAYCAAL 380
Db 321 LRDAKLDAKAOIHDLVVGSGSTRIPKVKLLQDFFNGRDLKSNINPEAAYGAAYCAAL 380
QY 381 MGDKSENVODLLLDVAPLSLGLTAGVMTALIKRNSTIPTKQTOIFTTYSDNQGVLI 440
Db 381 MGDKSENVODLLLDVAPLSLGLTAGVMTALIKRNSTIPTKQTOIFTTYSDNQGVLI 440
QY 441 QVEYGERAMT 450
Db 441 QVEYGERAMT 450

RESULT 5
HS7L_CERAE STANDARD; PRT; 638 AA.
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Heat shock 70 kDa protein 1.
GN HSPAL.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690;
RA Salins I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

```

CC or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch).  
 CC -----  
 DR EMBL: X70684; CAAS0019.1; -  
 DR HSP: P08107; 1H0.  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR ProDom: PD000089; Hsp70; 1.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family.  
 DR KW  
 DR SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;  
 SO  
 Query Match 27.3%; Score 175; DB 1; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-169;  
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 EDFPNRLVNHFEFFKRRKKKDISONKRAVRLRTACERAKRTSSSTQASLEIDSLFEG 290  
 DB 229 EDFPNRLVNHFEFFKRRKKKDISONKRAVRLRTACERAKRTSSSTQASLEIDSLFEG 288  
 QY 291 IDFTYSTRAFEBELCSDFRSTLEPEYKALRDAKLDKAQTHDLVVGSTRIPKVKLT 350  
 DB 289 IDFTYSTRAFEBELCSDFRSTLEPEYKALRDAKLDKAQTHDLVVGSTRIPKVKLT 348  
 QY 351 QDFPENGDLKSNIPDEAVAYGAAYVQAAILMGDKSENVODLLLDVAPLSIGLET 405  
 DB 349 QDFPENGDLKSNIPDEAVAYGAAYVQAAILMGDKSENVODLLLDVAPLSIGLET 403  
 RESULT 6  
 HS71\_RAT STANDARD; PRT; 641 AA.  
 ID HS71\_RAT  
 AC Q07439; P42853;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Heat shock 70 kDa protein 1/2 (HSP70.1/2).  
 GN HSP70-1 AND HSP70-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94096443; PubMed=8271311;  
 RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,  
 RA Massa S.M., Sharp F.R.:  
 RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal  
 RT and injured rat brain.";  
 RT J. Neurosci. Res. 36:325-335(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LTM.1W/GUN;  
 RX MEDLINE=95012453; PubMed=7927536;  
 RA Walter L., Rauh F., Guenther E.:  
 RT "Comparative analysis of the three major histocompatibility complex-  
 RT linked heat shock protein 70 (Hsp70) genes of the rat.";  
 RT Immunogenetics 40:325-330(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=94368874; PubMed=8086479;  
 RA Lisowska K., Krawczyk Z., Widiak W., Wolniczka P., Wisniewski J.:  
 RT "Cloning, nucleotide sequence and expression of rat heat inducible  
 RT hsp70 gene.";  
 RT Biochim. Biophys. Acta 1219:64-72(1994).  
 CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC OF NEARLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES

CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -!- INDUCTION: BY HEAT SHOCK.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
 CC  
 DR EMBL: L16764; AA017441.1; -  
 DR EMBL: X77208; CAAS4423.1; -  
 DR EMBL: X74207; CAAS4422.1; -  
 DR EMBL: X74271; CAAS2328.1; -  
 DR HSP: P08107; 1H0.  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR ProDom: PD000089; Hsp70; 1.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family.  
 DR KW  
 DR CONFLICT 71 72  
 FT CONFLICT 227 227 D -> H (IN REF. 3).  
 FT CONFLICT 408 408 G -> A (IN REF. 3).  
 SO SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;  
 Query Match 17.8%; Score 114; DB 1; Length 641;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-107;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 313 TLEPEYKALRDAKLDKAQTHDLVVGSTRIPKVKLLQDFPENGDLKSNIPDEAVAYG 372  
 DB 313 TLEPEYKALRDAKLDKAQTHDLVVGSTRIPKVKLLQDFPENGDLKSNIPDEAVAYG 372  
 QY 373 AAYVQAAILMGDKSENVODLLLDVAPLSIGLETAGVMTALIKRSTIPTKOTQ 426  
 DB 373 AAYVQAAILMGDKSENVODLLLDVAPLSIGLETAGVMTALIKRSTIPTKOTQ 426  
 RESULT 7  
 HS71\_MOUSE STANDARD; PRT; 641 AA.  
 ID HS71\_MOUSE  
 AC P17879; O61689;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN HSPAL OR HSP70A1 OR HSP70-1 OR HCP70.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=90236310; PubMed=2332169;  
 RA Hunt C., Calderwood S.:  
 RT "Characterization and sequence of a mouse hsp70 gene and its  
 RT expression in mouse cell lines.";  
 RT Gene 87:199-204(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94357449; PubMed=8076831;  
 RA Perry M.D., Aujame L., Shiang S., Moran L.A.:  
 RT "Structure and expression of an inducible HSP70-encoding gene from  
 RT Mus musculus.";

```

RL Gene 146:273-278(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M35021; AAA37864.1; -
DR EMBL; M76613; AAA57233.1; -
DR PIR; JH0095; JH0095.
DR HSP; P08107; 1HUO.
DR MGD; MGI:99517; HSP70-1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70.1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70.1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
KW CONFLICT 342 342 A -> R (IN REF. 1).
FT CONFLICT 627 627 P -> PP (IN REF. 1).
FT VARIANT 1 1
SQ SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;

Query Match 15.8%; Score 101; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 5e-94;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 PVTNAVITPAYFNDOSORATKAGIAGIAGLVRIINEPTAAIAVGLDRTGCGENVL 197
DB 138 PVTNAVITPAYFNDOSORATKAGIAGIAGLVRIINEPTAAIAVGLDRTGCGENVL 197
QY 198 FDLGGSTFVVSILITIDGIFEVKATAGTHLGGEDFDNRLV 238
DB 198 FDLGGSTFVVSILITIDGIFEVKATAGTHLGGEDFDNRLV 238

RESULT 8
HS73_MOUSE
ID HS73_MOUSE STANDARD; PRT; 420 AA.
AC Q61696; Q61697;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Heat shock 70 kDa protein 3 (HSP70.3) (Fragment).
GN HSP70-3 OR HSP70A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86111900; PubMed=2668009;
RA Love D.G., Moran L.A.;
RT "Molecular cloning and analysis of DNA complementary to three mouse
RL J. Biol. Chem. 261:2102-2112(1986).
RN [2]
RP SEQUENCE OF 155-420 FROM N.A.
RX MEDLINE=94357449; PubMed=8076831;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;

```

```

RT "Structure and expression of an inducible HSP70-encoding gene from
RL Mus musculus."
CC Gene 146:273-278(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12571; AAA57234.1; -
DR EMBL; M12572; AAA57235.1; -
DR HSP; P08109; 1CKR.
DR MGD; MGI:96244; Hsp70-3.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70.1.
DR ProDom; PD000089; Hsp70.1.
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
KW NON TER 1 1
FT VARIANT 188 188 V -> G.
SQ SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;

Query Match 12.5%; Score 80; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 7e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 DLYLVGSTRIRPVOKLDDFNGRDLNKSINPDENVANGAQAIIIMGDKSENVOLL 392
DB 112 DLYLVGSTRIRPVOKLDDFNGRDLNKSINPDENVANGAQAIIIMGDKSENVOLL 171
QY 393 LLDVAPLSLGLTAGGVMTA 412
DB 172 LLDVAPLSLGLTAGGVMTA 191

RESULT 9
HS71_ORYLA
ID HS71_ORYLA STANDARD; PRT; 639 AA.
AC Q918F9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70-1).
GN Oryzias latipes (Medaka fish) (Japanese ricefish).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=794311; PubMed=12571;
RA Naruse K., Sakuragi M.;
RT "Medaka Hsp70 gene cloning."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF286875; AAF91485.1; -  
DR HSSP; P08109; ICKR.  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70.1  
DR PRINTS; PR00301; HEATSHOCK70.  
DR ProDom; PD000089; HSP70.1.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock; Multigene family.  
SO SEQUENCE 639 AA; 70350 MW; 610B7E0DC0EB0534 CRC64;  
  
Query Match 8.9%; Score 57; DB 1; Length 639;  
Best Local Similarity 100.0%; Pred. No. 2,2e-49;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 IGIDLGTTSCVGVFGHGKVEIINDDGNRTTPSVAFPTDTERLIGDAKNOVALNP 63  
Db 9 IGIDLGTTSCVGVFGHGKVEIINDDGNRTTPSVAFPTDTERLIGDAKNOVALNP 65  
|||||  
  
RESULT 10  
HS72\_MOUSE STANDARD; PRT; 633 AA.  
ID HS72\_MOUSE  
AC P17156;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2).  
GN HSPA2 OR HSP70-2 OR HCP70.2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=88302212; PubMed=3405224;  
RA Zakeri Z.F., Wolgemuth D.J., Hunt C.R.;  
RT "Identification and sequence analysis of a new member of the mouse  
RT HSP70 gene family and characterization of its unique cellular and  
RT developmental pattern of expression in the male germ line."  
RL Mol. Cell. Biol. 8:2925-2932(1988).  
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
CC -1- DEVELOPMENTAL STAGE: SPECIFICALLY EXPRESSED IN PROPHAGE STAGE  
CC OR METOISTS.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M20567; AAA37859.1; -  
DR PIR; S10859; S10859.  
DR HSSP; P19120; IATR.  
DR MGD; MGI:96243; Hsp70-2.  
DR InterPro: IPR001023; Hsp70.

DR Pfam; PF00012; HSP70.1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR ProDom; PD000089; HSP70.1.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family.  
SO SEQUENCE 633 AA; 69740 MW; E7F9040F2AB138DD CRC64;  
  
Query Match 8.6%; Score 55; DB 1; Length 633;  
Best Local Similarity 100.0%; Pred. No. 2,4e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 AIGIDLGTTCVGVFGHGKVEIINDDGNRTTPSVAFPTDTERLIGDAKNOVA 60  
Db 7 AIGIDLGTTCVGVFGHGKVEIINDDGNRTTPSVAFPTDTERLIGDAKNOVA 61  
|||||  
  
RESULT 11  
HS72\_RAT STANDARD; PRT; 633 AA.  
ID HS72\_RAT  
AC P14659;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2) (Testis-  
DE specific heat shock protein-related) (HST).  
GN HSPA2 OR HS70.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=90122930; PubMed=1688714;  
RA Wisniewski J., Kordula T., Krawczyk Z.;  
RT "Isolation and nucleotide sequence analysis of the rat  
RT testis-specific major heat-shock protein (HSP70)-related gene."  
RL Biochim. Biophys. Acta 1048:93-99(1990).  
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X15705; CAA37335.1; -  
DR PIR; S08211; S08211.  
DR HSSP; P19120; 3HSC.  
DR InterPro: IPR001023; Hsp70.  
DR Pfam; PF00012; HSP70.1  
DR PRINTS; PR00301; HEATSHOCK70.  
DR ProDom; PD000089; HSP70.1.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family;  
KW Spermatogenesis.  
SO SEQUENCE 633 AA; 69528 MW; 6878CA5C2EBF7DA CRC64;  
  
Query Match 8.6%; Score 55; DB 1; Length 633;

Best Local Similarity 100.0%; Pred. No. 2.4e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AIGIDIGTTCVGVFGHGKVEIIANDQGNRTTPSYAFDTERRLLGDAKNOVA 60  
DB 7 AIGIDIGTTCVGVFGHGKVEIIANDQGNRTTPSYAFDTERRLLGDAKNOVA 61

RESULT 12  
HS70\_CHICK STANDARD; PRT; 634 AA.

AC P08106; 01-AUG-1988 (rel. 08, Created)  
DT 01-AUG-1988 (rel. 08, Last sequence update)  
DT 01-FEB-1994 (rel. 28, Last annotation update)  
DE Heat shock 70 kDa protein (HSP70).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86304452; PubMed=3017995;  
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;  
RT "Organization, nucleotide sequence, and transcription of the chicken  
HSP70 gene."  
RL J. Biol. Chem. 261:12692-12699(1986).  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: J02579; AAA4825.1; -  
DR PIR: A25646; A25646.  
DR HSSP: P08109; 1CKR.  
DR InterPro: IPR001023; Hsp70.  
DR Pfam: PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PRODOM: PD000089; Hsp70; 1.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock; Multigene family.  
SQ SEQUENCE 634 AA; 69750 MW; 4270F7E0BD365AEB CRC64;

Query Match 8.6%; Score 55; DB 1; Length 634;  
Best Local Similarity 100.0%; Pred. No. 2.4e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AIGIDIGTTCVGVFGHGKVEIIANDQGNRTTPSYAFDTERRLLGDAKNOVA 60  
DB 7 AIGIDIGTTCVGVFGHGKVEIIANDQGNRTTPSYAFDTERRLLGDAKNOVA 61

RESULT 13  
HS72\_HUMAN STANDARD; PRT; 639 AA.

AC P54652; 015508; Q9UE78;  
DT 01-OCT-1996 (rel. 34, Created)  
DT 01-OCT-1996 (rel. 34, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95130116; PubMed=7829106;  
RA Bonycastle L.L.C., Yu C.-E., Hunt C.R., Trask B.J., Clancy K.P.,  
RA Weber J.L., Patterson D., Schellenberg G.D.;  
RT "Cloning, sequencing, and mapping of the human chromosome 14 heat  
RT shock protein gene (HSPA2)."  
RL Genomics 23:85-93(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Goralski T.J., Krensky A.M.;  
RL Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.

RN [3]  
RP SEQUENCE OF 1-126 FROM N.A.  
RX MEDLINE=95152505; PubMed=7849706;  
RA Roux A.-F., Nguyen V.-T., Squire J.A., Cox D.W.;  
RT "A heat shock gene at 14q22: mapping and expression."  
RL Hum. Mol. Genet. 3:1819-1822(1994).  
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: L26336; AAA52698.1; -  
DR EMBL: U56725; AAD11466.1; -  
DR EMBL: U10149; AAC50076.1; -  
DR HSSP: P19120; 3HSC.  
DR GeneW: HGNC:5235; HSPA2.  
DR MIM: 140560; -  
DR InterPro: IPR001023; Hsp70.  
DR Pfam: PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PRODOM: PD000089; Hsp70; 1.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family.  
FT CONFLICT 54 MISSING (IN REF. 3).  
FT CONFLICT 266 L -> S (IN REF. 2).  
SQ SEQUENCE 639 AA; 70021 MW; 3851755494E7B729 CRC64;

Query Match 8.6%; Score 55; DB 1; Length 639;  
Best Local Similarity 100.0%; Pred. No. 2.4e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AIGIDIGTTCVGVFGHGKVEIIANDQGNRTTPSYAFDTERRLLGDAKNOVA 60  
DB 7 AIGIDIGTTCVGVFGHGKVEIIANDQGNRTTPSYAFDTERRLLGDAKNOVA 61

RESULT 14  
HS73\_RAT STANDARD; PRT; 641 AA.

AC P55063;  
DT 01-OCT-1996 (rel. 34, Created)  
DT 01-OCT-1996 (rel. 34, Last sequence update)  
DT 01-OCT-1996 (rel. 34, Last annotation update)  
DE Heat shock 70 kDa protein 3 (HSP70.3).  
OS Rattus norvegicus (Rat).  
GN HSP70-3.



```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-LEM.1W/GUN;
RX MEDLINE=95012453; Pubmed=7927536;
RA Walter L., Rauh F., Guenther E.;
RT "Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (Hsp70) genes of the rat.";
RL Immunogenetics 40:325-330(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X77209; CAA54424.1; -
DR HSSP; P08107; IHUO.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF000012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70549 MW; 8C77AA9FD98B9252 CRC64;

Query Match 8.6%; Score 55; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.4e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AIGIDLGTTSCVGFQHGKVEIIANDGNTTSPSYAFTDTERLIGDAKNAVA 60
DB 8 AIGIDLGTTSCVGFQHGKVEIIANDGNTTSPSYAFTDTERLIGDAKNAVA 62

RESULT 15
HSP70_HUMAN STANDARD; PRT; 641 AA.
ID HS7H_HUMAN
AC P34931; O9UCM1;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heat shock 70 kDa protein 1-HOM (HSP70-HOM).
GN HSP70.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91055806; Pubmed=1700760;
RA Milner C.M., Campbell R.D.;
RT "Structure and expression of the three MHC-linked HSP70 genes.";
RL Immunogenetics 32:242-251(1990).
RP SEQUENCE FROM N.A.
RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,

```

```

RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
RT region.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP VARIANT MET-493.
RX MEDLINE=92406261; Pubmed=1356099;
RA Milner C.M., Campbell R.D.;
RT "Polymorphic analysis of the three MHC-linked HSP70 genes.";
RL Immunogenetics 36:357-362(1992).
CC -1- INDUCTION: NOT INDUCED BY HEAT SHOCK.
CC -1- MISCELLANEOUS: ENCODED IN THE MHC-II COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M59829; AAA63228.1; -
DR EMBL; AF134726; AAD21817.1; -
DR PIR; B45871; B45871.
DR HSSP; P08107; IHUO.
DR Genew; HGNC:5234; HSP70.
DR MIM; 140559; -
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF000012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Multigene family; Polymorphism.
FT VARIANT 493 493 T->M.
FT CONFLICT 408 408 V->A (IN REF. 2).
FT CONFLICT 424 424 P->T (IN REF. 2).
SQ SEQUENCE 641 AA; 70399 MW; SCEPF58C9CF8EE55 CRC64;

Query Match 8.6%; Score 55; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.4e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AIGIDLGTTSCVGFQHGKVEIIANDGNTTSPSYAFTDTERLIGDAKNAVA 60
DB 8 AIGIDLGTTSCVGFQHGKVEIIANDGNTTSPSYAFTDTERLIGDAKNAVA 62

```

Search completed: December 4, 2002, 16:51:59  
 Job time : 15 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:47:18 : Search time 39 Seconds

(Without alignments)  
2190.094 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 641  
Sequence: 1 MAKAAAGIDLTGTYSCVGV.....FGAGPKPGSGSGPTIEVD 641

Scoring table:

Capop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_101002.\*  
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2004.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	641	100.0	641	19	AAW54349
2	641	100.0	641	21	AAW54349
3	641	100.0	641	22	AAW54349
4	641	100.0	641	22	AAW54349
5	624	97.3	624	21	AAW54349
6	624	97.3	624	21	AAW54349
7	624	97.3	624	21	AAW54349
8	624	97.3	624	21	AAW54349
9	624	97.3	624	21	AAW54349
10	624	97.3	624	21	AAW54349

11	244	38.1	244	21	AAW54349
12	205	32.0	640	11	AAW54349
13	168	26.2	168	22	AAW54349
14	168	26.2	168	22	AAW54349
15	168	26.2	168	22	AAW54349
16	168	26.2	168	22	AAW54349
17	168	26.2	168	22	AAW54349
18	168	26.2	168	22	AAW54349
19	168	26.2	168	22	AAW54349
20	168	26.2	168	22	AAW54349
21	168	26.2	168	22	AAW54349
22	168	26.2	168	22	AAW54349
23	135	21.1	136	22	AAW54349
24	101	15.8	641	14	AAW54349
25	101	15.8	641	14	AAW54349
26	100	15.6	554	21	AAW54349
27	100	15.6	554	21	AAW54349
28	92	14.4	92	21	AAW54349
29	71	11.1	137	21	AAW54349
30	60	9.4	647	11	AAW54349
31	55	8.6	633	14	AAW54349
32	55	8.6	633	14	AAW54349
33	53	8.3	120	21	AAW54349
34	53	8.3	212	22	AAW54349
35	53	8.3	292	22	AAW54349
36	53	8.3	451	22	AAW54349
37	53	8.3	646	11	AAW54349
38	53	8.3	646	11	AAW54349
39	53	8.3	646	20	AAW54349
40	53	8.3	646	20	AAW54349
41	53	8.3	646	21	AAW54349
42	53	8.3	646	21	AAW54349
43	53	8.3	646	22	AAW54349
44	53	8.3	646	22	AAW54349
45	53	8.3	646	23	AAW54349

#### ALIGNMENTS

RESULT 1	AAW54349
ID	AAW54349 standard; protein: 641 AA.
XX	AAW54349;
AC	14-AUG-1998 (first entry)
DT	XX
XX	Human heat shock 70 kD protein 1.
DE	XX
XX	Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
KW	2D gel electrophoresis; detection.
KW	XX
OS	Homo sapiens.
PN	W09810291-A1.
XX	XX
PD	12-MAR-1998.
XX	XX
PF	05-SEP-1997; 97WO-GB02394.
PR	08-APR-1997; 97GB-0007132.
PR	06-SEP-1996; 96GB-0018600.
XX	XX
PA	(CLIN-) CENT CLINICAL & BASIC RES.
PI	Byrjalsen I, Fey SJ, Larsen P;
XX	XX
DR	WPI; 1998-207057/18.
XX	XX
PT	Biochemical markers of human endometrium - useful for, e.g.
PT	diagnosis of hyperplasia and adenocarcinoma
XX	XX

Hsp70 C-terminal 2  
Homo sapiens HSP ( Peptide #3013 enco  
Peptide #3042 enco  
Protein #2959 enco  
Human brain expres  
Human bone marrow  
Peptide #2986 enco  
Peptide #3071 enco  
Peptide #2947 enco  
Human peptide enco  
Human heat shock p  
Human polypeptide  
Mature mouse sperm  
Rat heat shock pro  
Human heat shock p  
Hsp70 C-terminal 9  
Human cancer assoc  
Xenopus laevis HSP  
Mouse SLIP1 homolo  
Gallus gallus HSP  
Human secreted pro  
Novel human diagno  
Novel human diagno  
Novel human diagno  
Rat HSP (ratHsp70)  
Heat shock cognate  
Human heat shock c  
Mouse heat shock c  
Mouse heat shock p  
Human heat shock p  
Human Hsp70 family  
Human heat shock p  
Heat shock protein

PS Disclosure; Page 19; 77pp; English.

XX proteins AAW54349-W54364 are examples of proteins produced in the  
CC endometrium during the hyperplasia, adenocarcinoma or proliferative  
CC phase of the endometrium. The presence and quantities of these proteins  
CC can be detected using 2D gel electrophoresis and quantitation of cell lysates.  
CC The proteins can be used as biochemical markers to detect the phase of  
CC the endometrium and can be measured in body fluids, obviating the need  
CC for endometrial biopsies.

XX Sequence 641 AA;

Query Match 100.0%; Score 641; DB 19; Length 641;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKAAAGIDLGTTTSCVGFQHGKVEIITANDGNTTTPSYAFTDTERLIGDAKNQVA 60  
DB 1 MAKAAAGIDLGTTTSCVGFQHGKVEIITANDGNTTTPSYAFTDTERLIGDAKNQVA 60  
QY 61 LNPONTVFDAKRLIGKRFDPVQSDMKHMPQVINDGKPKQVSYKGETKAFYPEEIS 120  
DB 61 LNPONTVFDAKRLIGKRFDPVQSDMKHMPQVINDGKPKQVSYKGETKAFYPEEIS 120  
QY 121 SWVLTKMKEIAEAYLGYPVTNAVITVPAYFNDQKATKAGVIAGLNLVRLIINEPTAA 180  
DB 121 SWVLTKMKEIAEAYLGYPVTNAVITVPAYFNDQKATKAGVIAGLNLVRLIINEPTAA 180  
QY 181 IAYGLDRTGGERNVLIIFDLGGSTFVSLITIDGIFEVATAGDTHLGGEDFDNRLVNH 240  
DB 181 IAYGLDRTGGERNVLIIFDLGGSTFVSLITIDGIFEVATAGDTHLGGEDFDNRLVNH 240  
QY 241 FVEEFKRHKKDISOINKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFYTSTTRA 300  
DB 241 FVEEFKRHKKDISOINKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFYTSTTRA 300  
QY 301 RFEELCSDLFRSTLPEVEKALRDADKQIHDVLVVGSTRIIPKQKLLQDFPNRDLN 360  
DB 301 RFEELCSDLFRSTLPEVEKALRDADKQIHDVLVVGSTRIIPKQKLLQDFPNRDLN 360  
QY 361 KSIINPDEAVAYGAAYOAALIMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420  
DB 361 KSIINPDEAVAYGAAYOAALIMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420  
QY 421 PTKQTOFTTYSNQPGLVLIQVEGERAMTKDNNLLGRFELSGIPPARPGVPOIEVTFDI 480  
DB 421 PTKQTOFTTYSNQPGLVLIQVEGERAMTKDNNLLGRFELSGIPPARPGVPOIEVTFDI 480  
QY 481 DANGILNVTATDKSTGKANKITTTNDKRLSKEIEIRAVOAEKRYKAEDVOERVSAN 540  
DB 481 DANGILNVTATDKSTGKANKITTTNDKRLSKEIEIRAVOAEKRYKAEDVOERVSAN 540  
QY 541 ALSYAFNMKSAVEDDEGLKKKISEADKKVYLDCOEYISLDANTLAEKDEFEHKKRELE 600  
DB 541 ALSYAFNMKSAVEDDEGLKKKISEADKKVYLDCOEYISLDANTLAEKDEFEHKKRELE 600  
QY 601 QVCNPIISGLYQAGPGPGFQAQGGKSGSGSPITIEVD 641  
DB 601 QVCNPIISGLYQAGPGPGFQAQGGKSGSGSPITIEVD 641

RESULT 2

AAAB23652  
ID AAAB23652 standard; protein; 641 AA.

XX AAAB23652;

XX 05-JAN-2001 (first entry)

XX Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.

XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
KW Immune response; infectious disease; malaria; cytotoxic T cell;

KW cytostatic; immunostimulant; cellular immune response inducer;  
KW protozoacide; leukaemia; cancer.

XX Homo sapiens.

XX WO200049041-A1.

XX 24-AUG-2000.

XX 18-FEB-2000; 2000MO-JP00941.

XX 19-FEB-1999; 99JP-0041535.

XX (SUME) SUMITOMO ELECTRIC IND CO.

XX Shinbara N, udono H, Yui K;

XX WPI; 2000-543748/49.

PT Fused protein capable of inducing cellular immune response, useful as  
PT active ingredient for drug compositions in preventing and/or treating  
PT infectious diseases such as malaria or cancer -  
PS Claim 3; Page 46-48; 72pp; Japanese.

CC The present invention describes a fused protein (1) prepared from a  
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
CC shock protein. Also described are: (1) a drug composition containing (1)  
CC as active ingredient; (2) a DNA encoding (1); (3) an expression vector  
CC containing the DNA of (2); and (4) a transformant which can retain the  
CC expression vector of (3). (1) has cytostatic, immunostimulant and  
CC protozoacide activities, and can be used as a cellular immune response  
CC inducer. The protein is useful as an active ingredient for drug  
CC compositions in preventing and/or treating infectious diseases such as  
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
CC The present sequence represents a specifically claimed heat shock  
CC protein for use in a fused protein of the present invention.

XX Sequence 641 AA;

Query Match 100.0%; Score 641; DB 21; Length 641;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKAAAGIDLGTTTSCVGFQHGKVEIITANDGNTTTPSYAFTDTERLIGDAKNQVA 60  
DB 1 MAKAAAGIDLGTTTSCVGFQHGKVEIITANDGNTTTPSYAFTDTERLIGDAKNQVA 60  
QY 61 LNPONTVFDAKRLIGKRFDPVQSDMKHMPQVINDGKPKQVSYKGETKAFYPEEIS 120  
DB 61 LNPONTVFDAKRLIGKRFDPVQSDMKHMPQVINDGKPKQVSYKGETKAFYPEEIS 120  
QY 121 SWVLTKMKEIAEAYLGYPVTNAVITVPAYFNDQKATKAGVIAGLNLVRLIINEPTAA 180  
DB 121 SWVLTKMKEIAEAYLGYPVTNAVITVPAYFNDQKATKAGVIAGLNLVRLIINEPTAA 180  
QY 181 IAYGLDRTGGERNVLIIFDLGGSTFVSLITIDGIFEVATAGDTHLGGEDFDNRLVNH 240  
DB 181 IAYGLDRTGGERNVLIIFDLGGSTFVSLITIDGIFEVATAGDTHLGGEDFDNRLVNH 240  
QY 241 FVEEFKRHKKDISOINKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFYTSTTRA 300  
DB 241 FVEEFKRHKKDISOINKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFYTSTTRA 300  
QY 301 RFEELCSDLFRSTLPEVEKALRDADKQIHDVLVVGSTRIIPKQKLLQDFPNRDLN 360  
DB 301 RFEELCSDLFRSTLPEVEKALRDADKQIHDVLVVGSTRIIPKQKLLQDFPNRDLN 360  
QY 361 KSIINPDEAVAYGAAYOAALIMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420  
DB 361 KSIINPDEAVAYGAAYOAALIMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420

```
QY 421 PTKQOIFFTYSDNQPGLVIOYVEGERAMTKDNLLGFEELSGIPPARGVQIETVEDI 480
|||||
Dd 421 PTKQOIFFTYSDNQPGLVIOYVEGERAMTKDNLLGFEELSGIPPARGVQIETVEDI 480
QY 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOAEKKADEVQREVSASN 540
|||||
Dd 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOAEKKADEVQREVSASN 540
QY 541 ALESTAFNMKSAVEDEGLKGISADKKKVLDKCOEVIISWLDANTLAKDEFEHKKRLE 600
|||||
Dd 541 ALESTAFNMKSAVEDEGLKGISADKKKVLDKCOEVIISWLDANTLAKDEFEHKKRLE 600
QY 601 QVCNPIISGLYQAGGPGGFGAGGPKGSGSGPTIEVD 641
|||||
Dd 601 QVCNPIISGLYQAGGPGGFGAGGPKGSGSGPTIEVD 641

RESULT 3
AAE12986
ID AAE12986 standard; Protein: 641 AA.
XX
AC AAE12986;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human Hsp70 family homologue, Hsp71.
XX
KW Heat shock protein; HSP; HSP peptide-binding fragment; HSPF; vaccine;
KW cytotoxic T cell response; hepatitis virus; herpes simplex virus;
KW human immunodeficiency virus; bacteria; Mycobacteria; Rickettsia;
KW protozoa; Leishmania; Trypanosoma; intracellular parasite; Chlamydia;
KW sarcoma; carcinoma; cancer; human; Hsp70 homologue; Hsp71.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Binding-site 391..615
FT Binding-site /note="Peptide binding domain"
FT Binding-site 396..502
FT Domain /note="P-helix motif"
FT Domain 402..442
FT /note="Central core of peptide binding domain"
PN US2001034042-A1.
XX
PD 25-OCT-2001.
XX
PF 12-JAN-2001; 2001US-0759010.
XX
PR 20-JAN-2000; 2000US-0488393.
XX
PA (SRIV/) SRIVASTAVA P K.
PI
PI Silvastava PK;
XX
DR WPI; 2001-656559/75.
XX
PT Vaccine compositions for vaccinating against cancers and infections,
PT comprises peptide-binding fragments (PBFs) of heat shock proteins
PT (HSPs) and non-covalent complexes of PBFs of HSPs and antigenic
PT molecules -
XX
PS Disclosure; Fig 1C; 39pp; English.
XX
CC The invention relates to pharmaceutical compositions comprising
CC peptide binding fragments of heat shock proteins (HSPs) and non-
CC covalent complexes of HSP peptide-binding fragments (HSPF) in non-
CC covalent association with antigenic molecules. Vaccines comprising
CC peptide fragments of the invention may be used to stimulate an
CC immune response, in particular cytotoxic T cell responses against
CC cells infected with viruses (including hepatitis type A, B and C,
CC influenza, varicella, adenovirus, herpes simplex (HSV) type I and
CC type II, rinderpest rhinovirus, echovirus, rotavirus, respiratory
```

```
CC syncytial virus, mumps virus, papova virus, papilloma virus,
CC adenovirus, cytomegalovirus, echinovirus, hantavirus, coxsackie virus,
CC measles virus, rubella virus, polio virus, HIV-I and HIV-II;
CC bacteria including (including Mycobacteria, Rickettsia, Mycoplasma,
CC Neisseria and Legionella); protozoa (including Leishmania, Kokzidia
CC and Trypanosoma) and intracellular parasites (including Chlamydia and
CC Rickettsia). The vaccines may be used to treat cancers such as human
CC sarcomas and carcinomas, pancreatic cancer, breast cancer, ovarian
CC cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma,
CC adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma,
CC papillary carcinoma, papillary adenocarcinomas, medullary carcinoma,
CC cystadenocarcinoma, bronchogenic carcinoma, renal cell carcinoma,
CC hepatoma, bile duct carcinoma, choriocarcinoma, seminoma and embryonal
CC carcinoma. The present sequence is human Hsp70 family homologue, Hsp71.
XX
SQ Sequence 641 AA:
Query Match 100.0%; Score 641; DB 22; Length 641:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTSPVAFDTERRLIGDAKNQVA 60
|||||
Dd 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTSPVAFDTERRLIGDAKNQVA 60
QY 61 LNPQTVFADAKRLIGRKRGDPVYQSDMKHMPQVINDGDKPKVQYSYKGTAKFPEELS 120
|||||
Dd 61 LNPQTVFADAKRLIGRKRGDPVYQSDMKHMPQVINDGDKPKVQYSYKGTAKFPEELS 120
QY 121 SMVLTKMEIEAAYLGYPVNAVITVPVYFNDQSRQAKDAGVLAGLWLRITNEPTAA 180
|||||
Dd 121 SMVLTKMEIEAAYLGYPVNAVITVPVYFNDQSRQAKDAGVLAGLWLRITNEPTAA 180
QY 181 IAYGLDRTGGERNVLIPLDGGTFDVSILITDGIFFVKATAGPTHLIGEDFDNRLYNH 240
|||||
Dd 181 IAYGLDRTGGERNVLIPLDGGTFDVSILITDGIFFVKATAGPTHLIGEDFDNRLYNH 240
QY 241 FVEEFKRHHKDISONKRAVRLTRACERAKRTSSSQASLETDSLPREGIDFYSTR 300
|||||
Dd 241 FVEEFKRHHKDISONKRAVRLTRACERAKRTSSSQASLETDSLPREGIDFYSTR 300
QY 301 RFEELCSDLFRSTLEPVEKALRDADAKQIHDVLVVGSGTRIPVKQRLDQFENGRLDN 360
|||||
Dd 301 RFEELCSDLFRSTLEPVEKALRDADAKQIHDVLVVGSGTRIPVKQRLDQFENGRLDN 360
QY 361 KSIINDEAVAGAAVQAAILMGDKSENVODLLLDVAPLSGLETFAGVMTALIKRNSTI 420
|||||
Dd 361 KSIINDEAVAGAAVQAAILMGDKSENVODLLLDVAPLSGLETFAGVMTALIKRNSTI 420
QY 421 PTKQOIFFTYSDNQPGLVIOYVEGERAMTKDNLLGFEELSGIPPARGVQIETVEDI 480
|||||
Dd 421 PTKQOIFFTYSDNQPGLVIOYVEGERAMTKDNLLGFEELSGIPPARGVQIETVEDI 480
QY 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOAEKKADEVQREVSASN 540
|||||
Dd 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEEIERMVOAEKKADEVQREVSASN 540
QY 541 ALESTAFNMKSAVEDEGLKGISADKKKVLDKCOEVIISWLDANTLAKDEFEHKKRLE 600
|||||
Dd 541 ALESTAFNMKSAVEDEGLKGISADKKKVLDKCOEVIISWLDANTLAKDEFEHKKRLE 600
QY 601 QVCNPIISGLYQAGGPGGFGAGGPKGSGSGPTIEVD 641
|||||
Dd 601 QVCNPIISGLYQAGGPGGFGAGGPKGSGSGPTIEVD 641

RESULT 4
AAB82534
ID AAB82534 standard; Protein: 641 AA.
XX
AC AAB82534;
XX
DT 17-SEP-2001 (first entry)
```

```

XX Human heat shock protein Hsp71.
DE
XX Hsp71; human; heat shock protein; immunotherapy; therapy; cancer;
KW infection; vaccine.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Binding-site 391..615
FT /note="peptide-binding domain"
FT Region 395..502
FT /note="beta-helix motif"
FT Binding-site 400..440
FT /note="peptide-binding core"
XX
XX WO200152791-A2.
XX
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US01781.
XX
XX 20-JAN-2000; 2000US-0488393.
XX
XX (UYCO-) UNIV CONNECTICUT HEALTH CENT.
XX
XX Srivastava PK;
XX
XX WPI; 2001-457506/49.
XX
XX
XX Pharmaceutical composition, used to treat or prevent infection or
XX cancer, comprises a complex comprising a heat shock protein-binding
XX fragment associated with a molecule displaying antigenicity of an
XX infectious agent or cancer cell -
XX
XX
XX Claim 46; Fig 1C; 106pp; English.
XX
XX
XX The present sequence is that of human heat shock protein (HSP)
XX Hsp71, an inducible form of a Hsp70 family protein. The invention
XX relates to complexes of peptide-binding fragments of HSPs with
XX antigenic molecules and their use in immunotherapy for the treatment
XX of infectious diseases and cancer. Claimed methods of treating or
XX preventing cancer/infectious disease involve culturing a cancer
XX cell/infectious cell transformed with a nucleic acid encoding a HSP
XX peptide-binding domain, recovering complexes of the HSP fragments
XX noncovalently associated with peptides from the cancer cell/infectious
XX cell, and administering the recovered complexes. These methods can
XX use Hsp71 peptide-binding fragments comprising amino acids 391-615
XX and 400-440 of the present sequence, i.e. the peptide-binding
XX domain and peptide-binding core.
XX
XX
XX Sequence 641 AA:

```

```

Query Match 100.0%; Score 641; DB 22; Length 641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 MAKAAIGIDGTTSCVGFQHKVEIITANOGNRTTSSYAFDTRELIIDAKNOYA 60
DB 1 MAKAAIGIDGTTSCVGFQHKVEIITANOGNRTTSSYAFDTRELIIDAKNOYA 60
OY 61 LNPQTVDFAKRLIGRKFDPVQSDMKHMPPOVINDGDKPKVOYSYKETAPEETS 120
DB 61 LNPQTVDFAKRLIGRKFDPVQSDMKHMPPOVINDGDKPKVOYSYKETAPEETS 120
OY 121 SMVLTMRKEIAEAYLGYPVTNAVITVPAYFENDSORQATKAGVIAGLVNLRITNEPTAA 180
DB 121 SMVLTMRKEIAEAYLGYPVTNAVITVPAYFENDSORQATKAGVIAGLVNLRITNEPTAA 180
OY 181 IAYGIDRNGKGRNVLIDPLGGGTDFVSILITDDGIFEVKATAGTHLGGEPDNRLVN 240
DB 181 IAYGIDRNGKGRNVLIDPLGGGTDFVSILITDDGIFEVKATAGTHLGGEPDNRLVN 240

```

```

OY 241 FVEEFKHKHKIDISQNKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFYTSITRA 300
DB 241 FVEEFKHKHKIDISQNKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFYTSITRA 300
OY 301 REBELCSDLFRSTLEPEVEKALDPAKQIHDVLYVGGSTRIPKQKILQDFNCRDIN 360
DB 301 REBELCSDLFRSTLEPEVEKALDPAKQIHDVLYVGGSTRIPKQKILQDFNCRDIN 360
OY 361 KSIINPEAAVGAOAAIIMGDKSENVODLILDVAPISLIGETGGVMTLIRKNSIT 420
DB 361 KSIINPEAAVGAOAAIIMGDKSENVODLILDVAPISLIGETGGVMTLIRKNSIT 420
OY 421 PKQTQIFFTYSBNDQGVLIQVEGERAMTKNNLIGRELSGIPPAQVQIEVTFDI 480
DB 421 PKQTQIFFTYSBNDQGVLIQVEGERAMTKNNLIGRELSGIPPAQVQIEVTFDI 480
OY 481 DANGILNVTATDKSTGKAKKITITNDKGLSKFEIERMVAEKYKAEDPEVOREVSAN 540
DB 481 DANGILNVTATDKSTGKAKKITITNDKGLSKFEIERMVAEKYKAEDPEVOREVSAN 540
OY 541 ALESYAFNMKSAVEDEGLKGISEADKKRVLDKCOEIVISMLDANTLAEKDEFHKKKE 600
DB 541 ALESYAFNMKSAVEDEGLKGISEADKKRVLDKCOEIVISMLDANTLAEKDEFHKKKE 600
OY 601 QVCNPIISGLIYOGAGGPGGFGAOGPKGSGSGPTIEVD 641
DB 601 QVCNPIISGLIYOGAGGPGGFGAOGPKGSGSGPTIEVD 641

```

```

RESULT 5
AAB23252
ID AAB23252 standard; Protein; 624 AA.
XX
XX AAB23252;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human Hsp72 (heat shock protein 72).
XX
XX
XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
XX expression modulator; JNK phosphatase inhibitor; antiproliferative;
XX drug screening; cancer; leukemia; lymphoma; solid tumour; sarcoma;
XX carcinoma; breast cancer; prostate cancer; premalignant condition.
XX
XX Homo sapiens.
XX
XX WO200054814-A1.
XX
XX 21-SEP-2000.
XX
XX 17-MAR-2000; 2000WO-US07350.
XX
XX 18-MAR-1999; 99US-0125046.
XX
XX (PHYL-) PHYLOGENY INC.
XX
XX Volloch VZ, Sherman M;
XX
XX WPI; 2000-647056/62.
XX
XX N-PSDB; AAA97541.
XX
XX Identifying compounds that inhibit proliferation of cells and capable
XX of modulating the expression of heat shock protein 72 gene and/or
XX activity of Hsp72 useful for treating cancers such as leukemia,
XX lymphoma
XX
XX Examples; Fig 16B; 77pp; English.
XX
XX The invention relates to a novel method of identifying compounds that
XX inhibit proliferation of cells comprising contacting a test compound with
XX a cell which overexpresses Hsp72 (heat shock protein 72), and determining
XX if the test compound inhibits activity or expression of Hsp72.
XX
XX Optionally, Hsp72 is contacted with the test compound under optimum
XX

```

conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp27-mediated JNK phosphatase activation, comprising contacting a test compound with a cell which expresses Hsp27, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of Hsp27 or JNK phosphatase activity. The compounds identified as inhibitors of Hsp27 or JNK phosphatase activity are useful for inhibiting the proliferation of cells. Modulation of the activity of the JNK phosphatase or Hsp27 is used to treat a proliferative disorder such as cancers (e.g., leukemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp27 activity can also be administered to treat pre-malignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp27 function are administered to a patient having a disease or disorder mediated by an increase of Hsp27 expression or activity relative to normal levels. The present sequence represents human Hsp27 used in the exemplifications of the invention.

Sequence 624 AA;

Query Match	97.3%;	Score 624;	DB 21;	Length 624;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 624;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MAAAAGIDIGTGYSCVGVGHOKHVELIANDOGNRTPTSVATPTDRLLIGDAAKNOVA	60
Db	1	MAKAAAGIDIGTGYSCVGVGHOKHVELIANDOGNRTPTSVATPTDRLLIGDAAKNOVA	60
QY	61	LNPNQVFAKRLLRIGRKRGDPVVGOSDKMHFPOYIINDDKRVGVSKGEKAFYPEIS	120
Db	61	LNPNQVFAKRLLRIGRKRGDPVVGOSDKMHFPOYIINDDKRVGVSKGEKAFYPEIS	120
QY	121	SMVLTKKKEIEMAYLGIPVTNAVITVPAYFENDSORQATKQAGVITAGLVNRIINEPTAA	180
Db	121	SMVLTKKKEIEMAYLGIPVTNAVITVPAYFENDSORQATKQAGVITAGLVNRIINEPTAA	180
QY	181	IAYGLDRFGKGERNVLIIPDLGGGFFDYSILITIDGIEFVKATAGDTHLGEGDPNNRLVNH	240
Db	181	IAYGLDRFGKGERNVLIIPDLGGGFFDYSILITIDGIEFVKATAGDTHLGEGDFNNRLVNH	240
QY	241	FVEEFKRKHKKDISQNKRAVRLRTACERAKRTLSSSTQASLEIDSLEFEGIDIFYSTIRA	300
Db	241	FVEEFKRKHKKDISQNKRAVRLRTACERAKRTLSSSTQASLEIDSLEPEGIDIFYSTIRA	300
QY	301	REFEELCSLEFSTLEPEVKALARDKALDKAQIHDVLVVGGSRTIRKVOQLLODFNGRBLN	360
Db	301	REFEELCSLEFSTLEPEVKALARDKALDKAQIHDVLVVGGSRTIRKVOQLLODFNGRBLN	360
QY	361	KSINPDEAVAAGAIVOAAIIMGDKSENVODLLLDVAPLSGLETAGCVMTALIKRNSTI	420
Db	361	KSINPDEAVAAGAIVOAAIIMGDKSENVODLLLDVAPLSGLETAGCVMTALIKRNSTI	420
QY	421	PTKQTQIETTYSDNOGVLIQVYEGGERAMTKNNLLGFEELSGIIPPAIRGVQIETVEDI	480
Db	421	PTKQTQIETTYSDNOGVLIQVYEGGERAMTKNNLLGFEELSGIIPPAIRGVQIETVEDI	480
QY	481	DANGLVANTAYDKSGCKRANKTTIINDGRLSKEELERFVNOCAEKYKADVEQRRERSKXN	540
Db	481	DANGLVANTAYDKSGCKRANKTTIINDGRLSKEELERFVNOCAEKYKADVEQRRERSKXN	540
QY	541	ALBESYAFNMKSAVEDEGLKGRISADKKKVLDKQOEVSIMLDAMTIAEKDEFEHKKRLE	600
Db	541	ALBESYAFNMKSAVEDEGLKGRISADKKKVLDKQOEVSIMLDAMTIAEKDEFEHKKRLE	600
QY	601	QVCNPIISGLYQAGAGGPGGSGFGA 624	
Db	601	QVCNPIISGLYQAGAGGPGGSGFGA 624	

RESULT 6  
AAB23653

ID	AAB23653 standard; protein; 640 AA.
XX	
AC	AAB23653;
XX	
DT	05-JAN-2001 (first entry)
XX	
DE	Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
XX	
KM	ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW	immune response; infectious disease; malaria; cytotoxic T cell;
KX	cytostatic; immunostimulant; cellular immune response inducer;
RN	protozoacide; leukaemia; cancer.
XX	
OS	Homo sapiens.
PN	WO200049041-A1.
XX	
PD	24-Aug-2000.
XX	
PF	18-FEB-2000; 2000MO-JP00941.
XX	
PR	19-FEB-1999; 99JP-0041535.
XX	
PA	(SOME ) SUMITOMO ELECTRIC IND CO.
P1	Shinbara N, Udono H, Yui K;
DR	WPI; 2000-543748/49.
XX	
PT	Fused protein capable of inducing cellular immune response, useful as
PT	active ingredient for drug compositions in preventing and/or treating
PS	infectious diseases such as malaria or cancer
XX	
XX	Claim 3; Page 49-52; 72pp; Japanese.
CC	
CC	The present invention describes a fused protein (I) prepared from a
CC	peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC	cytotoxic T cells and a protein containing the ATPase domain of a heat
CC	shock protein. Also described are: (1) a drug composition containing (I)
CC	as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC	containing the DNA of (2); and (4) a transformant which can retain the
CC	expression vector of (3). (I) has cyrostatic, immunostimulant and
CC	protozoacide activities, and can be used as a cellular immune response
CC	inducer. The protein is useful as an active ingredient for drug
CC	compositions in preventing and/or treating infectious diseases such as
CC	malaria or cancer e.g. to provide systemic immunity against Leukaemia.
CC	The present sequence represents a specifically claimed heat shock
CC	protein for use in a fused protein of the present invention.
XX	
SO	Sequence 640 AA:
Query Match	64.3%; Score 412; DB 21; Length 640;
Best Local Similarity	99.7%; Pred. No. 0;
Matches 632; Conservative	0; Mismatches 1; Indels 1; Gaps 1
OY	8 GIDLGTTSCVGFQHGKVEIIANDGNGFTSPSYAFTDTERLIGDAKNVOALNPONTV 67
DB	GTTTSCVGVFQHGKVEIIANDGNGRTTSPSYAFTDTERLIGDAKNVOALNPONTU 67
OY	68 FPAKLRLGKKFGDDPVVQSOMKHMPROYINDGSKPKVOYSYKGKTRAFYEELISSMYLTGM 127
DB	FPAKLRLGKKFGDDPVVQSOMKHMPROYINDGSKPKVOYSYKGKTRAFYEELISSMYLTGM 127
OY	128 KEIAEVLGYCPTNTNAVITYPAFYFNDSORPATDAGVIAGLANLVRIINEPTAAIAVGLDR 187
DB	KEIAEVLGYCPTNTNAVITYPAFYFNDSORPATDAGVIAGLANLVRIINEPTAAIAVGLDR 187
OY	186 TGKGERNNVLIFDLGGTFDVSIITIDDGIFEVKATAGDTHLGGEDFDNLVNHFEFFKR 247
DB	TGKGERNNVLIFDLGGTFDVSIITIDDGIFEVKATAGDTHLGGEDFDNLVNHFEFFKR 247
OY	248 KKKKDISONKRAVRRLRTPACERAKRTLSSSTOASLEISDFEGIDFYITSITARRPEELCS 307
DB	KKKKDISONKRAVRRLRTPACERAKRTLSSSTOASLEISDFEGIDFYITSITARRPEELCS 307

```

Db 248 KHKKIDISQNKRAVRRLKTCERAKRLSSSTQASLEIDSLFEGIDYTSITRARFEELCS 307
QY 308 DLFIRSTLEPEYKALRPDAKLDAQIHDVLVYGSGSTRIPKVOKLLODFENGRLDKSINPDE 367
Db 308 DLFIRSTLEPEYKALRPDAKLDAQIHDVLVYGSGSTRIPKVOKLLODFENGRLDKSINPDE 367
QY 368 AVAYGAAVQAAILMGDKSENVODLLLDVAPLSLGLFETAGGVMTALIKRNSTIPTKQTOI 427
Db 368 AVAYGAAVQAAILMGDKSENVODLLLDVAPLSLGLFETAGGVMTALIKRNSTIPTKQTOI 427
QY 428 FTTYSNONGPVLQYVEGEFAMTKDNLLGRFELSGIPRPRGVPOIEVFPDIDANGILN 487
Db 428 FTTYSNONGPVLQYVEGEFAMTKDNLLGRFELSGIPRPRGVPOIEVFPDIDANGILN 486
QY 488 VTATDSTGKANKITTTNDKGRLSKEIERMVOEAEKYKAEDVORERYSANKNALESYAF 547
Db 487 VTATDSTGKANKITTTNDKGRLSKEIERMVOEAEKYKAEDVORERYSANKNALESYAF 546
QY 548 NMSKSAVEDEGLKGISEADKKVLDKQCEVISMLDANTLAEKDFEHKRELEBOVCNPIT 607
Db 547 NMSKSAVEDEGLKGISEADKKVLDKQCEVISMLDANTLAEKDFEHKRELEBOVCNPIT 606
QY 608 SGLYOGAGGPGGPGFAQGCPKGGSGSPITIEVD 641
Db 607 SGLYOGAGGPGGPGFAQGCPKGGSGSPITIEVD 640

```

## RESULT 7

AAy88409

-ID AAY88409 standard; Protein; 554 AA.

XX AAY88409;

DT 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

KW Human: heat shock protein; HSP70; chromosome 6p21.3-22; stress;

KM chromosome 14q22-24; transcription; rheumatism; schizophrenia;

KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

XX N-PSDB: AAA15621.

XX Abnormal transcription of intracellular HSP70mRNA under acute and

XX chronic continuous load of stress in a human being and its application

XX Examples; Fig 2; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid

XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22

XX and 14q22-24. The invention relates to the abnormal transcription of

XX intracellular HSP70mRNA under acute and chronic stress load in a human.

XX The abnormal transcription of HSP70 can be used in the improvement of

XX stress and response and diagnosis of stress diseases including

XX rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

XX Query Match 52.0%; Score 333; DB 21; Length 554;

XX

Best local Similarity 99.6%; Pred. No. 2,3e-313;  
Matches 553; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

QY 87 MKHMPFOVINDGKPKPVQVSYKGETKAFYPEELSSWVLTFRMKRLAELAYGYPTNVAVIV 146
Db 1 MKHMPFOVINDGKPKPVQVSYKGETKAFYPEELSSWVLTFRMKRLAELAYGYPTNVAVIV 60
QY 147 PAYFNDSORQATDAGVIAGLANLRIINEPTAAIYVAGLDRTGKGRNVLIPLDGGTFPD 206
Db 61 PAYFNDSORQATDAGVIAGLANLRIINEPTAAIYVAGLDRTGKGRNVLIPLDGGTFPD 120
QY 207 VSLITFDIDGIFEYKATAGDTHLGEDPDNRLVNHVEVEEKRKHKDISQNKRAVRRLRTA 266
Db 121 VSLITFDIDGIFEYKATAGDTHLGEDPDNRLVNHVEVEEKRKHKDISQNKRAVRRLRTA 180
QY 267 CERAKRPLSSSTQASLEIDSLFEGIDYTSITRARFEELCSDLFRLSTLEPEYKALRDAKL 326
Db 181 CERAKRPLSSSTQASLEIDSLFEGIDYTSITRARFEELCSDLFRLSTLEPEYKALRDAKL 240
QY 327 DKAQIHDVLVYGSGSTRIPKVOKLLODFENGRLDKSINPDEAVAYGAAVQAAILMGDKSE 386
Db 241 DKAQIHDVLVYGSGSTRIPKVOKLLODFENGRLDKSINPDEAVAYGAAVQAAILMGDKSE 300
QY 387 NVODLLLDVAPLSLGLFETAGGVMTALIKRNSTIPTKQTOIEFTYSDNPGVLIQYEGE 446
Db 301 NVODLLLDVAPLSLGLFETAGGVMTALIKRNSTIPTKQTOIEFTYSDNPGVLIQYEGE 360
QY 447 RAMFKDNINLLGRFELSGIPRPRGVPOIEVFPDIDANGILNVTATDSTGKANKITTTND 506
Db 361 RAMFKDNINLLGRFELSGIPRPRGVPOIEVFPDIDANGILNVTATDSTGKANKITTTND 419
QY 507 KGRLSKEIERMVOEAEKYKAEDVORERYSANKNALESYAFNMSKSAVEDEGLKGISEAD 566
Db 420 KGRLSKEIERMVOEAEKYKAEDVORERYSANKNALESYAFNMSKSAVEDEGLKGISEAD 479
QY 567 KKKVLDKQCEVISMLDANTLAEKDFEHKRELEBOVCNPITISGLYOGAGGPGGPGFAQG 626
Db 480 KKKVLDKQCEVISMLDANTLAEKDFEHKRELEBOVCNPITISGLYOGAGGPGGPGFAQG 539
QY 627 PKGGSGSPITIEVD 641
Db 540 PKGGSGSPITIEVD 554

```

## RESULT 8

AAy88410

-ID AAY88410 standard; Protein; 554 AA.

XX AAY88410;

DT 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

KW Human: heat shock protein; HSP70; chromosome 6p21.3-22; stress;

KM chromosome 14q22-24; transcription; rheumatism; schizophrenia;

KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

XX N-PSDB: AAA15622.

XX



PT Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
XX  
XX  
PS Disclosure; Fig 3; 11pp; Japanese.  
XX  
CC This sequence represents the human heat shock protein HSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
SQ Sequence 554 AA;  
  
Query Match 52.0%; Score 333; DB 21; Length 554;  
Best Local Similarity 99.6%; Pred. No. 2.3e-313;  
Matches 553; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
  
QY 87 MKHMPFYINGDKPKVQVSYKGETKAFYPEISSMVLTKKETAELVIGPVTNAVITY 146  
DB 1 MKHMPFYINGDKPKVQVSYKGETKAFYPEISSMVLTKKETAELVIGPVTNAVITY 60  
  
QY 147 PAYFNDGROATKAGVAGTAGLNLVRLINEPTAAATAGLDRTGKERVILFDLGGGTFD 206  
DB 61 PAYFNDGROATKAGVAGTAGLNLVRLINEPTAAATAGLDRTGKERVILFDLGGGTFD 120  
  
QY 207 VSILTIDGIFEVKATAGDTHLGGEDFNDRLVNHFEVEFKRHKHKKDISQNKRAVRLTA 266  
DB 121 VSILTIDGIFEVKATAGDTHLGGEDFNDRLVNHFEVEFKRHKHKKDISQNKRAVRLTA 180  
  
QY 267 CERAKRTSSSTQASLEIDSLFEGIDFTSTTRAFEECLSDLFSTLEPEKALRDAL 326  
DB 181 CERAKRTSSSTQASLEIDSLFEGIDFTSTTRAFEECLSDLFSTLEPEKALRDAL 240  
  
QY 327 DKAQIHDLVLYGVGSTRIPKVKQLDGFNGRDNLKNSINPDEAVAGAAVQAAIILMGDSE 386  
DB 241 DKAQIHDLVLYGVGSTRIPKVKQLDGFNGRDNLKNSINPDEAVAGAAVQAAIILMGDSE 300  
  
QY 387 NVQDLLLDVAPLSLIGETAGGVMTALIKRNSTIPTKOTQIFTTYSDNOFVLLQVYEGE 446  
DB 301 NVQDLLLDVAPLSLIGETAGGVMTALIKRNSTIPTKOTQIFTTYSDNOFVLLQVYEGE 360  
  
QY 447 RAMTKDNLLGRFELSGTPAPRGVPOLEVPEDIDANGLNLTADKSTGRANKTTITND 506  
DB 361 RAMTKDNLLGRFELSGTPAPRGVPOLEVPEDIDANGLNLTADKSTGRANKTTITND 419  
  
QY 507 KGRLSKEIEIRNVOEAERYKKADEVOERVSANKNALESYAFNMKSAVDEGLKGRKISEAD 566  
DB 420 KGRLSKEIEIRNVOEAERYKKADEVOERVSANKNALESYAFNMKSAVDEGLKGRKISEAD 479  
  
QY 567 KKKVLDKCOEYISWLDANTLAEKDEFEHKRELEQVCNP11SGLYQAGGPGGFGAGQ 626  
DB 480 KKKVLDKCOEYISWLDANTLAEKDEFEHKRELEQVCNP11SGLYQAGGPGGFGAGQ 539  
  
QY 627 PKGGSGSGPTIEVD 641  
DB 540 PKGGSGSGPTIEVD 554  
  
RESULT 9  
AAW10065  
ID AAW10065 standard; Protein; 640 AA.  
XX  
XX AAW10065;  
XX  
DT 24-Oct-1997 (first entry)  
XX  
DE Human heat shock protein 70.  
XX  
KW Human; heat shock protein 70; HSP70; primer; probe; detection;  
KW intracellular; abnormal transcription; acute; chronic; sustained;

KW stress.  
XX  
OS Homo sapiens.  
XX  
PN JP08322577-A.  
XX  
PD 10-DEC-1996.  
XX  
PF 01-JUN-1995; 95JP-0158581.  
XX  
PR 01-JUN-1995; 95JP-0158581.  
XX  
PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX  
DR WPI; 1997-081088/08.  
XX  
DR N-PSDB; AAT56086.  
XX  
PT Detection of abnormal transcription of HSP70 mRNA - using HSP70  
PT specific primer or probe, used in detection of human acute and  
PT chronic sustained stress load  
XX  
PS Claim 1; Fig 1; 13pp; Japanese.  
XX  
CC The cDNA encoding the present sequence, human heat shock protein 70  
CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
CC and 21. Primers and probes based on the HSP70 cDNA coding of  
CC sequence can be used to detect the abnormal transcription of  
CC intracellular HSP70 mRNA in human acute and chronic sustained  
CC stress load.  
XX  
SQ Sequence 640 AA;  
  
Query Match 46.2%; Score 296; DB 18; Length 640;  
Best Local Similarity 100.0%; Pred. No. 1.7e-277;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 GIDLSTYSCVGFPHGVEITANDQGNRTTPSYAFDTERLIGDAKNOVALNPONTY 67  
DB 8 GIDLSTYSCVGFPHGVEITANDQGNRTTPSYAFDTERLIGDAKNOVALNPONTY 67  
  
QY 68 FDKRLIRGRKFGDPVQSDMKHMPQVINDGDKPKVQVSYKGETKAFYPEISSMVLTKM 127  
DB 68 FDKRLIRGRKFGDPVQSDMKHMPQVINDGDKPKVQVSYKGETKAFYPEISSMVLTKM 127  
  
QY 128 KEIAAYIGPYPTNAVITVPAYFNDGROATKAGVAGTAGLNLVRLINEPTAAATAGGLDR 187  
DB 128 KEIAAYIGPYPTNAVITVPAYFNDGROATKAGVAGTAGLNLVRLINEPTAAATAGGLDR 187  
  
QY 188 TGKGRNVLIPLDGGGTFDVSILTTIDGIFEVKATAGDTHLGGEDFNDRLVNHFEVEFKR 247  
DB 188 TGKGRNVLIPLDGGGTFDVSILTTIDGIFEVKATAGDTHLGGEDFNDRLVNHFEVEFKR 247  
  
QY 248 KHKDISQNKRAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTSTTRAFEE 303  
DB 248 KHKDISQNKRAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFTSTTRAFEE 303  
  
RESULT 10  
AAW88408  
ID AAW88408 standard; Protein; 640 AA.  
XX  
XX AAW88408;  
XX  
DT 31-JUL-2000 (first entry)  
XX  
DE Human heat shock protein HSP70 amino acid sequence.  
XX  
KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW Chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome.  
XX  
OS Homo sapiens.  
XX

PN JP2000069999-A.  
XX  
XX 07-MAR-2000.  
XX  
XX 01-JUN-1995: 99JP-0257146.  
XX  
XX 01-JUN-1995: 95JP-0158581.  
XX  
XX (HOKE-) HOKEN KAGAKU KENKUSHO KK.  
XX  
XX WPI: 2000-264458/23.  
DR N-PSDB: AAA15620.  
XX  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX  
XX Claim 2: Fig 1: 11pp: Japanese.  
XX  
XX This sequence represents the human heat shock protein HSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 640 AA:  
SQ  
\* Query Match 40.7%; Score 261; DB 21; Length 640;  
Best local Similarity 99.7%; Pred. No. 1.3e-243;  
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 GIDLGTVSCVGFQHGKVEIINDDGNRTPTSVAFPTQNERLIGAAKQVALNPNQTV 67  
DB 8 GIDLGTVSCVGFQHGKVEIINDDGNRTPTSVAFPTQNERLIGAAKQVALNPNQTV 67  
QY 68 FDKRLIGRKGFGDPVVOQSMKHPFOVINDGDKPKVOVSFKGTAKAFYPREISSMVLTKM 127  
DB 68 FDKRLIGRKGFGDPVVOQSMKHPFOVINDGDKPKVOVSFKGTAKAFYPREISSMVLTKM 127  
QY 128 KEIAEAYLGYPVNAVITVPAYFNDSORQATKAGYAGLNVLRINEPTAAAIAYGLDR 187  
DB 128 KEIAEAYLGYPVNAVITVPAYFNDSORQATKAGYAGLNVLRINEPTAAAIAYGLDR 187  
QY 188 TGCGERNVLIFDLGGGFQVSIITIDGIFEVKATAGDTFLGGEEDNRLVNFVEBFKR 247  
DB 188 TGCGERNVLIFDLGGGFQVSIITIDGIFEVKATAGDTFLGGEEDNRLVNFVEBFKR 247  
QY 248 KHKKDISONKRAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFYTSITRAFEEELCS 307  
DB 248 KHKKDISONKRAVRLRTACERAKRTLSSTQASLEIDSLFEGIDFYTSITRAFEEELCS 307  
QY 308 DLFRLSLPEPEKALRDQAKLDKQIHDLYLVGSGTRIPKVKLLQDPFNGDLNKSINPDE 367  
DB 308 DLFRLSLPEPEKALRDQAKLDKQIHDLYLVGSGTRIPKVKLLQDPFNGDLNKSINPDE 367  
QY 368 AV 369  
DB 368 AV 369  
RESULT 11  
AAB09886  
ID AAB09886 standard; protein; 244 AA.  
XX  
XX AAB09886;  
AC  
XX  
DT 06-NOV-2000 (first entry)  
XX  
DE Hsp70 C-terminal 244 amino acid polypeptide sequence.  
XX  
KW Heat shock protein 70; Hsp70; NF-kappaB; transplant rejection;

KW autoimmune disease; inflammatory disease; cancer; vascular disease.  
XX  
XX Homo sapiens.  
XX  
XX WO200031113-A1.  
PN  
XX  
XX 02-JUN-2000.  
PD  
XX  
XX 17-NOV-1999: 99WO-US27244.  
PF  
XX 24-NOV-1998: 98US-0109872.  
PR  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Fujihara SM, Nadler SG;  
PI  
XX  
XX WPI: 2000-400029/34.  
DR  
XX  
XX Intracellular targeted delivery of compounds using the 70 kilodalton  
PT heat shock protein, useful in the treatment of transplant rejection,  
PT autoimmune diseases and cancer -  
XX  
XX Claim 6: page 17; 37pp; English.  
XX  
XX The present sequence is the C-terminal 244 amino acids of the 70kD heat  
CC shock protein (Hsp70). This sequence was used in a fusion protein with  
CC the p50 subunit of transcription factor NF-kappaB, the sequence of which  
CC is indicated in the specification as being SEQ ID NO: 1, but which is  
CC not given. This fusion protein was created in order to determine the  
CC ability of the Hsp70 sequence to direct other proteins into the cell. It  
CC was shown that Hsp70 fragments are able to direct other proteins into  
CC the cell, a feature which can be used in the treatment of transplant  
CC rejection, autoimmune diseases such as rheumatoid arthritis, multiple  
CC sclerosis, diabetes, asthma, inflammatory bowel disease, psoriasis,  
CC hepatitis, Graves' disease and viteligo, inflammatory diseases including  
CC osteoarthritis, pancreatitis and adult respiratory distress syndrome,  
CC cancer, vascular diseases (such as restenosis and atherosclerosis) and  
CC DNA and RNA viral replication diseases (including herpes).  
XX  
XX Sequence 244 AA:  
SQ  
Query Match 38.1%; Score 244; DB 21; Length 244;  
Best local Similarity 100.0%; Pred. No. 1.6e-227;  
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 398 PLSIGLETAGCVATLTKRSTIPTKOTLETTYSNQGVLQVYEGERAMTKDNNLIG 457  
DB 1 PLSIGLETAGCVATLTKRSTIPTKOTLETTYSNQGVLQVYEGERAMTKDNNLIG 60  
QY 458 RFEISGIPAPRGVPIEVTFDIDANGILNVATDSTGKANKITTTNDKGRLSKEIER 517  
DB 61 RFEISGIPAPRGVPIEVTFDIDANGILNVATDSTGKANKITTTNDKGRLSKEIER 120  
QY 518 MVOEAKRYKAEDEVQREBRYSAKNALSYAFNMKSAVEDELKKKISEADKKYLDQCEY 577  
DB 121 MVOEAKRYKAEDEVQREBRYSAKNALSYAFNMKSAVEDELKKKISEADKKYLDQCEY 180  
QY 578 ISWLDANTLAEKDFEKKRELPOVCNPIISGLYOGAGCGPGGFAOGCPKGGSGSGPTI 637  
DB 181 ISWLDANTLAEKDFEKKRELPOVCNPIISGLYOGAGCGPGGFAOGCPKGGSGSGPTI 240  
QY 638 EEYD 641  
DB 241 EEYD 244  
RESULT 12  
AAR03929  
ID AAR03929 standard; protein; 640 AA.  
XX  
XX AAR03929;  
AC  
XX  
DT 30-AUG-1990 (first entry)

```

XX DE Homo sapiens HSP (humhsp70).
XX KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT MISC-difference 640 /note= "residue given as "O" in specification"
XX PA
XX PN MO3002564-A.
XX PD 22-MAR-1990.
XX PF 12-SEP-1989; 89WO-0003955.
XX PR 12-SEP-1988; 88US-0243474.
XX PA (CODON-) CODON.
XX PI Dragon E, Faulds D, Sias S;
XX DR WPI: 1990-115820/15.
XX PT Proteins homologous to heat shock proteins from Trypanosoma cruzi - used
XX in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
XX PS Disclosure; Flg 2.1-2.14; 86pp; English.
XX CC According to the legend of Fig 2, the H. sapiens HSP sequence has
XX 641 amino acid residues, the sequence itself has only 640,
XX including "O" (?) at position 640.
XX CC Fig. 2 provides an alignment of heat shock proteins from a variety
XX of organisms: 1. M. hyopneumoniae (Mhysp70 - AAR03922);
XX 2. Bacillus megaterium (Bmehsp70 - AAR03923);
XX 3. E. coli (dha - AAR03924);
XX 4. T. cruzi (tc70kd - AAR03925);
XX 5. T. cruzi (AAR03926);
XX 6. Rat rattus (rathsp70 - AAR03927);
XX 7. Xenopus laevis (xl70 - AAR03928);
XX 8. Homo sapiens (humhsp70 - AAR03929);
XX 9. Gallus gallus (chkhsp70 - AAR03930);
XX 10. Zea mays (zmehsp70 - AAR03931);
XX 11. Serratia marcescens (smahsp70 - AAR03932).
XX The proteins having homology to hsp's of T. cruzi can be used in
XX vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
XX Mycobacteria species.
XX SQ Sequence 640 AA;
XX
Query Match 32.0%; Score 205; DB 11; Length 640;
Best Local Similarity 99.4%; Pred. No. 2,1e-189;
Matches 525; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

```

Db 328 KAOIHDLVVGSGSTRIPKVKLLODFENGRLNKSINPDEAVYGAAYAAIIMGDKSEN 387
Qy 388 VODILLDVAPLSLGLEFAGGMYTALIKRNSITPRTKQITFTYSDNPGVLIQYEEGR 447
Db 388 VODILLDVAPLSLGLEFAGGMYTALIKRNSITPRTKQITFTYSDNPGVLIQYEEGR 447
Qy 448 AMTKDNMLGRFELSGLIPAPRGVQIETFDIDANGILNATDRTSGKANKITITNDK 507
Db 448 AMTKDNMLGRFELSGLIPAPRGVQIETFDIDANGILNATDRTSGKANKITITNDK 506
Qy 508 GLSKKEEIERMVOEAKYKAEDVOERYSKNALESYAFAFNKSAVEDEGLGKISEADK 567
Db 507 GLSKKEEIERMVOEAKYKAEDVOERYSKNALESYAFAFNKSAVEDEGLGKISEADK 566
Qy 568 KKVLDKCOEIVISWLDANTLAEKDEFEHRKRELEJOVCNPIISGLYOGAG 615
Db 567 KKVLDKCOEIVISWLDANTLAEKDEFEHRKRELEJOVCNPIISGLYOGAG 614

RESULT 13
ABB30362
ID ABB30362 standard; Peptide: 168 AA.
AC ABB30362;
XX 01-FEB-2002 (first entry)
DT
DE Peptide #3013 encoded by breast cell single exon nucleic acid probe.
XX Human; microarray; single exon probe; gene expression; breast;
XX disease; cancer.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000662.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI: 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes,
XX useful for measuring gene expression in sample derived from human
XX breast, comprises number of single exon nucleic acid probes.
XX PS Claim 27; SEQ ID NO 13330; 327bp + sequence listing; English.
XX
The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and Bt 474 cells. The method involves contacting
CC the probes with a collection of detectably labeled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
than expressed sequence tag microarrays. The method is suitable for

```

CC rapid production of functional information from genomic sequence. The  
CC present sequence is a peptide encoded by a single exon nucleic acid  
CC probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
CC  
XX

Sequence 168 AA:

Query Match 26.2%; Score 168; DB 22; Length 168;  
Best Local Similarity 100.0%; Pred. No. 4.4e-154;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 IEVTFPIDANGILNVTATDKSTGKANKITTTNDKGRLSKEIERMVOEAKRYAEDEVQR 533  
DB 1 IEVTFPIDANGILNVTATDKSTGKANKITTTNDKGRLSKEIERMVOEAKRYAEDEVQR 60  
QY 534 ERYSAKNALESYAFNMKSAVEDEGLKGISEADKKVLDKQCVISWLDANTLAEKDEFE 593  
DB 61 ERYSAKNALESYAFNMKSAVEDEGLKGISEADKKVLDKQCVISWLDANTLAEKDEFE 120  
QY 594 HKRKELEQVCNPITISGLYGAGGPGGFGAQPCKGSGSGPTIEEVD 641  
DB 121 HKRKELEQVCNPITISGLYGAGGPGGFGAQPCKGSGSGPTIEEVD 168

## RESULT 14

ABB35536  
ID ABB35536 standard; Peptide; 168 AA.

AC ABB35536;

DT 04-FEB-2002 (first entry)

DE Peptide #3042 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-483447/52.

Human genome-derived single exon nucleic acid probes useful for  
analyzing gene expression in human fetal liver -

Claim 27; SEQ ID NO 28171; 639pp + sequence listing; English.

The invention relates to a single exon nucleic acid probe for  
measuring human gene expression in a sample derived from human foetal  
liver. The single exon nucleic acid probes may be used for predicting,  
measuring and displaying gene expression in samples derived from human  
fetal liver. The present sequence is a peptide encoded by a single exon  
nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the  
printed specification, but was obtained in electronic format directly

CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 168 AA:

Query Match 26.2%; Score 168; DB 22; Length 168;  
Best Local Similarity 100.0%; Pred. No. 4.4e-154;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 IEVTFPIDANGILNVTATDKSTGKANKITTTNDKGRLSKEIERMVOEAKRYAEDEVQR 533  
DB 1 IEVTFPIDANGILNVTATDKSTGKANKITTTNDKGRLSKEIERMVOEAKRYAEDEVQR 60  
QY 534 ERYSAKNALESYAFNMKSAVEDEGLKGISEADKKVLDKQCVISWLDANTLAEKDEFE 593  
DB 61 ERYSAKNALESYAFNMKSAVEDEGLKGISEADKKVLDKQCVISWLDANTLAEKDEFE 120  
QY 594 HKRKELEQVCNPITISGLYGAGGPGGFGAQPCKGSGSGPTIEEVD 641  
DB 121 HKRKELEQVCNPITISGLYGAGGPGGFGAQPCKGSGSGPTIEEVD 168

## RESULT 15

ABB20960  
ID ABB20960 standard; Protein; 168 AA.

AC ABB20960;

DT 23-JAN-2002 (first entry)

DE Protein #2959 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488899/53.

Single exon nucleic acid probes for analyzing gene expression in human  
hearts -

Claim 15; SEQ ID NO 22730; 530pp; English.

The present invention relates to single exon nucleic acid probes for  
measuring human gene expression in a sample derived from human heart (see  
ABA21535-ABA41305). The present sequence is a protein encoded by one such  
probe. The probes may be used for predicting, measuring and displaying  
gene expression in samples derived from the human heart via microarrays.  
By measuring gene expression, the probes are useful for predicting,  
diagnosing, grading, staging, monitoring and prognosing diseases of the  
human heart and vascular system e.g. cardiovascular disease,  
hypertension, cardiac arrhythmias and congenital heart disease.  
Note: The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format directly from WIPO



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:35:27 : Search time 39 Seconds  
(without alignments)  
2190.094 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 3263

Sequence: 1 MKAAMAGIDLGTTYSYCVG.....FGAGPKGGSGSGPTIEVD 641

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A.geneSeq\_101002.\*  
2: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT.\*  
3: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT.\*  
4: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT.\*  
5: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT.\*  
6: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT.\*  
7: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT.\*  
8: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT.\*  
9: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT.\*  
10: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT.\*  
11: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT.\*  
12: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT.\*  
13: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT.\*  
14: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT.\*  
15: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT.\*  
16: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT.\*  
17: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT.\*  
18: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT.\*  
19: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT.\*  
20: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT.\*  
21: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.\*  
22: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.\*  
23: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3263	100.0	641	19	AAW54349	Human heat shock 7
2	3263	100.0	641	21	AAAB3652	Human heat shock p
3	3263	100.0	641	22	AAAB12986	Human Hsp70 family
4	3263	100.0	641	22	AAAB25534	Human heat shock p
5	3242.5	99.4	640	21	AAAB23653	Human heat shock p
6	3229.5	99.0	640	18	AAAT0065	Human heat shock p
7	3229.5	99.0	640	21	AAAB8408	Human heat shock p
8	3211	98.4	640	21	AAAB03929	Homo sapiens HSP (
9	3172	97.2	624	21	AAAB3252	Human Hsp72 (heat
10	3130	95.9	641	14	AAAB3004	Mature mouse sperm

11	3125.5	95.8	642	21	AAAB23650	Rat heat shock pro
12	3093.5	94.8	640	21	AAAB88411	Human heat shock p
13	2862.5	87.7	646	20	AAAT74408	Mouse heat shock c
14	2862.5	87.7	646	21	AAAB3649	Mouse heat shock p
15	2859.5	87.6	646	19	AAW54364	Heat shock cognate
16	2859.5	87.6	646	20	AAAT7407	Human heat shock c
17	2859.5	87.6	646	21	AAAB3651	Human heat shock p
18	2859.5	87.6	646	22	AAAT2987	Human Hsp70 family
19	2859.5	87.6	646	22	AAAB2535	Human heat shock p
20	2859.5	87.6	646	23	AAAT5102	Heat shock protein
21	2859.5	87.6	890	21	AAAB2938	GFP-HSC70 fusion p
22	2837.5	87.0	646	11	AAAR03927	Rat HSP (ratHsp70)
23	2834.5	86.9	647	11	AAAR03928	Xenopus laevis HSP
24	2803.5	85.9	554	21	AAAB8409	Human heat shock p
25	2803.5	85.9	554	21	AAAB8410	Human heat shock p
26	2754.5	84.4	633	14	AAAR3002	Mouse SLIP homolo
27	2747.5	84.2	634	11	AAAR03930	Gallus gallus HSP
28	2747.5	84.2	643	23	AAAB48711	Human schizopren
29	2740	84.0	665	21	AAAB58386	Lung cancer associ
30	2737	83.9	651	22	AAAB60514	Drosophila melanog
31	2718	83.3	643	18	AAW22895	Marmoset Intracell
32	2692.5	82.5	554	21	AAAB8413	Human heat shock p
33	2664	81.6	641	22	AAAB71708	Drosophila melanog
34	2661.5	81.6	554	21	AAAB8412	Drosophila melanog
35	2524.5	77.4	620	11	AAAR03932	Human heat shock p
36	2502.5	76.7	656	18	AAW01638	Serratia marcescen
37	2465.5	75.6	646	21	AAAG53604	Candida albicans h
38	2439.5	74.8	629	22	AAAB67209	Arabidopsis thalia
39	2436.5	74.7	635	22	AAAB61529	Drosophila melanog
40	2423	74.3	646	11	AAAR03931	Zea mays HSP (mzh
41	2414.5	74.0	647	20	AAAT1380	T. gondii antigen
42	2414.5	74.0	647	22	AAAB49099	Toxoplasma gondii
43	2402	73.6	677	11	AAAR09418	Hsp70 antigen from
44	2388.5	73.2	676	9	AAAB80088	Sequence of 70kd p
45	2386.5	73.1	623	21	AAAG53605	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1  
AAW54349  
AAW54349 standard; protein: 641 AA.

AC AAW54349;  
XX  
XX 14-AUG-1998 (first entry)  
XX  
XX Human heat shock 70 kd protein 1.  
XX  
XX Endometrium: hyperplasia; adenocarcinoma: proliferative phase;  
XX 2d gel electrophoresis; detection.  
XX  
XX Homo sapiens.  
XX  
XX W09810291-A1.  
XX  
XX 12-MAR-1998.  
XX  
XX 05-SEP-1997; 97WO-GB02394.  
XX  
XX 08-APR-1997; 97GB-0007132.  
XX 06-SEP-1996; 96GB-0018600.  
XX  
XX (CLIN-) CENT CLINICAL & BASIC RES.  
XX  
XX Byrjalsen I, Fey ST, Larsen P;  
XX  
XX WPI: 1998-207057/18.  
XX  
XX Biochemical markers of human endometrium - useful for, e.g.  
XX diagnosis of hyperplasia and adenocarcinoma

PS Disclosure; Page 19; 77pp; English.

CC Proteins AAW54349-W54364 are examples of proteins produced in the  
CC endometrium during the hyperplasia, adenocarcinoma or proliferative  
CC phase of the endometrium. The presence and quantities of these proteins  
CC can be detected using 2D gel electrophoresis comparison of cell lysates.  
CC The proteins can be used as biochemical markers to detect the phase of  
CC the endometrium and can be measured in body fluids, obviating the need  
CC for endometrial biopsies.

XX Sequence 641 AA:

Query Match 100.0%; Score 3263; DB 19; Length 641;  
Best Local Similarity 100.0%; Pred. No. 1.4e-224;  
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKAAAGIDLTGTTSCVGFQHGKVEIIANDQGNRTTPSYAFDTERTLIGDAKNQYA 60  
DB 1 MAKAAAGIDLTGTTSCVGFQHGKVEIIANDQGNRTTPSYAFDTERTLIGDAKNQYA 60  
QY 61 LNPQNTVFDKRLIGKRFDPVQSDMKHMPFOVINDGDKPKVQSYKGTAFYPEEIS 120  
DB 61 LNPQNTVFDKRLIGKRFDPVQSDMKHMPFOVINDGDKPKVQSYKGTAFYPEEIS 120  
QY 121 SWLTKMKETIAEAYLGYPVTNAVITVPAYFNDQROATKAGVIAGLNLRIINEPTAA 180  
DB 121 SWLTKMKETIAEAYLGYPVTNAVITVPAYFNDQROATKAGVIAGLNLRIINEPTAA 180  
QY 181 IAVGLDRTGKERNVLIIFDLGGTFPVSLITIDDGIFEVKATGDPHLSGEDPDRNLVNH 240  
DB 181 IAVGLDRTGKERNVLIIFDLGGTFPVSLITIDDGIFEVKATGDPHLSGEDPDRNLVNH 240  
QY 241 FVEEFKRHKKDISONKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFTYSITRA 300  
DB 241 FVEEFKRHKKDISONKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFTYSITRA 300  
QY 301 REBELCSDLFRSTLPEVEKALDKAQIHDVLVVGSTRIAPKYOQLDQFFNGRDLN 360  
DB 301 REBELCSDLFRSTLPEVEKALDKAQIHDVLVVGSTRIAPKYOQLDQFFNGRDLN 360  
QY 361 KSNINPEAVAYGAOVAAILMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSIT 420  
DB 361 KSNINPEAVAYGAOVAAILMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSIT 420  
QY 421 PTKQQLFTTYSNDQGVLIQVYEGERAMTKDNLGRELSGIPRPRGVPQIEVTFDI 480  
DB 421 PTKQQLFTTYSNDQGVLIQVYEGERAMTKDNLGRELSGIPRPRGVPQIEVTFDI 480  
QY 481 DANGIILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYAEDEVQREYSAKN 540  
DB 481 DANGIILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYAEDEVQREYSAKN 540  
QY 541 ALESYAFNMKSAVEDGLGKISSEADKKVLDKCOEIVISLDANTLAEKDEFHKKRKE 600  
DB 541 ALESYAFNMKSAVEDGLGKISSEADKKVLDKCOEIVISLDANTLAEKDEFHKKRKE 600  
QY 601 QVCNPIISGLYOGAGGPGPGFAGQPKGSGSGPTIEEVD 641  
DB 601 QVCNPIISGLYOGAGGPGPGFAGQPKGSGSGPTIEEVD 641

RESULT 2

AAB23652  
ID AAB23652 standard; protein: 641 AA.

XX AAB23652;

XX 05-JAN-2001 (first entry)

XX Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.

XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
XX Immune response; infectious disease; malaria; cytotoxic T cell;

KW cytostatic; immunostimulant; cellular immune response inducer;  
KW protozoacide; leukaemia; cancer.

XX Homo sapiens.

XX WO200049041-A1.

XX 24-AUG-2000.

XX 18-FEB-2000; 2000MO-JP00941.

XX 19-FEB-1999; 99JP-0041535.

XX (SUME ) SUMITOMO ELECTRIC IND CO.

XX Shinbara N, Udono H, Yui K;

XX WPI; 2000-543748/49.

PT Fused protein capable of inducing cellular immune response, useful as  
PT active ingredient for drug compositions in preventing and/or treating  
PT infectious diseases such as malaria or cancer

PS Claim 3; Page 46-48; 72pp; Japanese.

CC The present invention describes a fused protein (1) prepared from a  
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
CC cytotoxic T cells and a protein containing the Arpase domain of a heat  
CC shock protein. Also described are: (1) a drug composition containing (1)  
CC as active ingredient; (2) a DNA encoding (1); (3) an expression vector  
CC containing the DNA of (2); and (4) a transformant which can retain the  
CC expression vector of (3). (1) has cytostatic, immunostimulant and  
CC protozoacide activities, and can be used as a cellular immune response  
CC inducer. The protein is useful as an active ingredient for drug  
CC compositions in preventing and/or treating infectious diseases such as  
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
CC The present sequence represents a specifically claimed heat shock  
CC protein for use in a fused protein of the present invention.

XX Sequence 641 AA:

Query Match 100.0%; Score 3263; DB 21; Length 641;  
Best Local Similarity 100.0%; Pred. No. 1.4e-224;  
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKAAAGIDLTGTTSCVGFQHGKVEIIANDQGNRTTPSYAFDTERTLIGDAKNQYA 60  
DB 1 MAKAAAGIDLTGTTSCVGFQHGKVEIIANDQGNRTTPSYAFDTERTLIGDAKNQYA 60  
QY 61 LNPQNTVFDKRLIGKRFDPVQSDMKHMPFOVINDGDKPKVQSYKGTAFYPEEIS 120  
DB 61 LNPQNTVFDKRLIGKRFDPVQSDMKHMPFOVINDGDKPKVQSYKGTAFYPEEIS 120  
QY 121 SWLTKMKETIAEAYLGYPVTNAVITVPAYFNDQROATKAGVIAGLNLRIINEPTAA 180  
DB 121 SWLTKMKETIAEAYLGYPVTNAVITVPAYFNDQROATKAGVIAGLNLRIINEPTAA 180  
QY 181 IAVGLDRTGKERNVLIIFDLGGTFPVSLITIDDGIFEVKATGDPHLSGEDPDRNLVNH 240  
DB 181 IAVGLDRTGKERNVLIIFDLGGTFPVSLITIDDGIFEVKATGDPHLSGEDPDRNLVNH 240  
QY 241 FVEEFKRHKKDISONKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFTYSITRA 300  
DB 241 FVEEFKRHKKDISONKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFTYSITRA 300  
QY 301 REBELCSDLFRSTLPEVEKALDKAQIHDVLVVGSTRIAPKYOQLDQFFNGRDLN 360  
DB 301 REBELCSDLFRSTLPEVEKALDKAQIHDVLVVGSTRIAPKYOQLDQFFNGRDLN 360  
QY 361 KSNINPEAVAYGAOVAAILMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSIT 420  
DB 361 KSNINPEAVAYGAOVAAILMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSIT 420



```

QY 421 PTKQTOIFTTYSNQPGLVIOYEGEERAMTKDNLLGREFELSGIPPARGVQOIEVTEDI 480
    |||||||
DB 421 PTKQTOIFTTYSNQPGLVIOYEGEERAMTKDNLLGREFELSGIPPARGVQOIEVTEDI 480
    |||||||
QY 481 DANGILNTATADKSTGKANKKITTNDKGRLSKEEIERMVOEAKYKADEVOERERSAKN 540
    |||||||
DB 481 DANGILNTATADKSTGKANKKITTNDKGRLSKEEIERMVOEAKYKADEVOERERSAKN 540
    |||||||
QY 541 ALESYAFNNKSAVEDEGLKGTISEADKKRVLDKCEVISMILANTLAERDEFEHRRKELE 600
    |||||||
DB 541 ALESYAFNNKSAVEDEGLKGTISEADKKRVLDKCEVISMILANTLAERDEFEHRRKELE 600
    |||||||
QY 601 QVCNPIISGLYOGAGGPGGFGAGGPKGSGSGSPPIIEVD 641
    |||||||
DB 601 QVCNPIISGLYOGAGGPGGFGAGGPKGSGSGSPPIIEVD 641
    |||||||

RESULT 3
AAE12986
ID AAE12986 standard; Protein: 641 AA.
XX
AC AAE12986;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human Hsp70 family homologue, Hsp71.
XX
KW Heat shock protein; HSP; HSP peptide-binding fragment; HSPF; vaccine;
KW cytotoxic T cell response; hepatitis virus; herpes simplex virus;
KW human immunodeficiency virus; bacteria; Mycobacteria; Rickettsia;
KW protozoa; Leishmania; Trypanosoma; intracellular parasite; Chlamydia;
KW sarcoma; carcinoma; cancer; human; Hsp70 homologue; Hsp71.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 391..615
FT Binding-site /note="peptide binding domain"
FT Binding-site 396..502
FT Domain /note="P-helix motif"
FT Domain 402..442
FT /note="Central core of peptide binding domain"
XX
PN US2001034042-A1.
XX
PD 25-OCT-2001.
XX
PF 12-JAN-2001; 2001US-0759010.
XX
PR 20-JAN-2000; 2000US-0488393.
XX
PA (SRIV/) SRIVASTAVA P K.
XX
PI Srivastava PK;
XX
WP: 2001-656559/75.
XX
DR
XX
PT Vaccine compositions for vaccinating against cancers and infections,
PT comprises peptide-binding fragments (PBPs) of heat shock proteins
PT (HSPs) and non-covalent complexes of PBPs of HSPs and antigenic
PT molecules -
XX
PS Disclosure: Fig 1C; 39pp; English.
XX
CC The invention relates to pharmaceutical compositions comprising
CC peptide binding fragments of heat shock proteins (HSPs) in non-
CC covalent complexes of HSP peptide-binding fragments (HSPF) and non-
CC covalent association with antigenic molecules. Vaccines comprising
CC peptide fragments of the invention may be used to stimulate an
CC immune response, in particular cytotoxic T cell responses against
CC cells infected with viruses (including hepatitis type A, B and C,
CC influenza, varicella, adenovirus, herpes simplex (HSV) type I and
CC type II, rinderpest rhinovirus, echovirus, rotavirus, respiratory

```

```

CC syncytial virus, mumps virus, papova virus, papilloma virus,
CC arbovirus, cytomegalovirus, echovirus, hantavirus, coxsackie virus,
CC measles virus, rubella virus, polio virus, HIV-1, and HIV-II;
CC bacteria including (including Mycobacteria, Rickettsia, Mycoplasma,
CC Neisseria and Legionella); protozoa (including Leishman, Kokidiola
CC and Trypanosoma) and intracellular parasites (including Chlamydia and
CC Rickettsia). The vaccines may be used to treat cancers such as human
CC sarcoma and carcinoma, pancreatic cancer, breast cancer, ovarian
CC cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma,
CC adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma,
CC papillary carcinoma, papillary adenocarcinomas, medullary carcinoma,
CC cystadenocarcinoma, bronchogenic carcinoma, renal cell carcinoma,
CC hepatoma, bile duct carcinoma, choriocarcinoma, seminoma and embryonal
CC carcinoma. The present sequence is human Hsp70 family homologue, Hsp71.
XX
SQ Sequence 641 AA;
XX
Query Match 100.0%; Score 3263; DB 22; Length 641;
Best Local Similarity 100.0%; Pred. No. 1,4e-224;
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAKAAAGIDIGTGYSCGVFQHGKVEIANDQNKRTTPSYVAFPTERTLIGDAAKNOYA 60
    |||||||
DB 1 MAKAAAGIDIGTGYSCGVFQHGKVEIANDQNKRTTPSYVAFPTERTLIGDAAKNOYA 60
    |||||||
QY 61 LNPONTVPDPAKRLIGRFGDPVQSDMKHMPPOVINDGKPRVOYSYKGETAFYPEETS 120
    |||||||
DB 61 LNPONTVPDPAKRLIGRFGDPVQSDMKHMPPOVINDGKPRVOYSYKGETAFYPEETS 120
    |||||||
QY 121 SVALTRMKRIATAYAGYPTNAVITVPAYFNOSORQATDAGVIGLANTLRITNEPTAA 180
    |||||||
DB 121 SVALTRMKRIATAYAGYPTNAVITVPAYFNOSORQATDAGVIGLANTLRITNEPTAA 180
    |||||||
QY 181 IAYGLDRGKGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEDFDRNLVNH 240
    |||||||
DB 181 IAYGLDRGKGERNVLIIFDLGGTFDVSILITIDGIFEVKATAGDTHLGEDFDRNLVNH 240
    |||||||
QY 241 FVEEERKRRKKKISQNKRAVRRLRTACERAKTLLSSSTQASLEISLPGIDFTYSITRA 300
    |||||||
DB 241 FVEEERKRRKKKISQNKRAVRRLRTACERAKTLLSSSTQASLEISLPGIDFTYSITRA 300
    |||||||
QY 301 REEELCSDFRSTLFEVEKALDPAKIDKQIHDLVYVGSTRLPKYOKLLODFPNGRDN 360
    |||||||
DB 301 REEELCSDFRSTLFEVEKALDPAKIDKQIHDLVYVGSTRLPKYOKLLODFPNGRDN 360
    |||||||
QY 361 KSINPDEAVAYGAAYQAAILMGDKSENVDLLLDVAPLSLGLTAGVMTALIKRNSTI 420
    |||||||
DB 361 KSINPDEAVAYGAAYQAAILMGDKSENVDLLLDVAPLSLGLTAGVMTALIKRNSTI 420
    |||||||
QY 421 PTKQTOIFTTYSNQPGLVIOYEGEERAMTKDNLLGREFELSGIPPARGVQOIEVTEDI 480
    |||||||
DB 421 PTKQTOIFTTYSNQPGLVIOYEGEERAMTKDNLLGREFELSGIPPARGVQOIEVTEDI 480
    |||||||
QY 481 DANGILNTATADKSTGKANKKITTNDKGRLSKEEIERMVOEAKYKADEVOERERSAKN 540
    |||||||
DB 481 DANGILNTATADKSTGKANKKITTNDKGRLSKEEIERMVOEAKYKADEVOERERSAKN 540
    |||||||
QY 541 ALESYAFNNKSAVEDEGLKGTISEADKKRVLDKCEVISMILANTLAERDEFEHRRKELE 600
    |||||||
DB 541 ALESYAFNNKSAVEDEGLKGTISEADKKRVLDKCEVISMILANTLAERDEFEHRRKELE 600
    |||||||
QY 601 QVCNPIISGLYOGAGGPGGFGAGGPKGSGSGSPPIIEVD 641
    |||||||
DB 601 QVCNPIISGLYOGAGGPGGFGAGGPKGSGSGSPPIIEVD 641
    |||||||

RESULT 4
AAB82534
ID AAB82534 standard; Protein: 641 AA.
XX
AC AAB82534;
XX
DT 17-SEP-2001 (first entry)

```

```

XX XX Human heat shock protein Hsp71.
DE XX
XX Hsp71: human: heat shock protein; immunotherapy; therapy; cancer;
KM Infection; vaccine.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Binding-site 391..615
FT /note="peptide-binding domain"
FT Region 395..502
FT /note="beta-helix motif"
FT Binding-site 400..440
FT /note="peptide-binding core"
XX
XX WO200152791-A2.
PD
PD 26-JUL-2001.
PD
PD 18-JAN-2001; 2001WO-US01781.
PF
PR 20-JAN-2000; 2000US-0488393.
XX
XX (UYCO-) UNIV CONNECTICUT HEALTH CENT.
PA
PA Srivastava PK;
PI
XX
XX WPI; 2001-457506/49.
XX
XX Pharmaceutical composition, used to treat or prevent infection or
PT cancer, comprises a complex comprising a heat shock protein-binding
PT fragment associated with a molecule displaying antigenicity of an
PT infectious agent or cancer cell -
XX
XX Claim 46; Fig 1C; 106pp; English.
XX
XX The present sequence is that of human heat shock protein (HSP)
CC Hsp71, an inducible form of a Hsp70 family protein. The invention
CC relates to complexes of peptide-binding fragments of HSPs with
CC antigenic molecules and their use in immunotherapy for the treatment
CC of infectious diseases and cancer. Claimed methods of treating or
CC preventing cancer/infectious disease involve culturing a cancer
CC cell/infectious cell transformed with a nucleic acid encoding a HSP
CC peptide-binding domain, recovering complexes of the HSP fragments
CC noncovalently associated with peptides from the cancer cell/infectious
CC cell, and administering the recovered complexes. These methods can
CC use Hsp71 peptide-binding fragments comprising amino acids 391-615
CC and 400-440 of the present sequence, i.e. the peptide-binding
CC domain and peptide-binding core.
CC
XX
XX Sequence 641 AA:
SQ
Query Match 100.0%; Score 3263; DB 22; Length 641;
Best Local Similarity 100.0%; Pred. No. 1.4e-224;
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAKAAAIGDGLGTTSCVGFQHGCKVETIIANDGQNRTPSYAFTDERLIGDAKNOVA 60
DB 1 MAFAAAIGDGLGTTSCVGFQHGCKVETIIANDGQNRTPSYAFTDERLIGDAKNOVA 60
QY 61 LNFQNTVFDAKRLIGKRFQSPVYVQSDMKHMPQVYINDGDKPKVOVSYKGETKAFYPEIS 120
DB 61 LNFQNTVFDAKRLIGKRFQSPVYVQSDMKHMPQVYINDGDKPKVOVSYKGETKAFYPEIS 120
QY 121 SMVLTKKKEIAEAYLGYPVNAVITVPAYFNDGSRQATKAGVYAGLVRLTINEPTAA 180
DB 121 SMVLTKKKEIAEAYLGYPVNAVITVPAYFNDGSRQATKAGVYAGLVRLTINEPTAA 180
QY 181 IAVGLDRTGGERNVLLFDLGGGTFDVSILITIDGIFEVKAATAGDTHLGSEDEPNRLVNH 240
DB 181 IAVGLDRTGGERNVLLFDLGGGTFDVSILITIDGIFEVKAATAGDTHLGSEDEPNRLVNH 240

```

```

QY 241 FVEEFKRKKHKDISQNKRAVRRLTACERAKRFLSSSTQASLEIDSLFESIDPFTSITRA 300
DB 241 FVEEFKRKKHKDISQNKRAVRRLTACERAKRFLSSSTQASLEIDSLFESIDPFTSITRA 300
QY 301 RFPELCSDLFRSTLEPEPKALRDAKIDKQITHLVLYGSGSTRIPKYOKLLQDFPNGRDLN 360
DB 301 RFPELCSDLFRSTLEPEPKALRDAKIDKQITHLVLYGSGSTRIPKYOKLLQDFPNGRDLN 360
QY 361 KSINPDEAVAYGAAYQAAIIMGDKSENVODLLLDVAPLSLGLFTAGVMTALIKRNSTI 420
DB 361 KSINPDEAVAYGAAYQAAIIMGDKSENVODLLLDVAPLSLGLFTAGVMTALIKRNSTI 420
QY 421 PTKOTQLETTYSDNQPCVLLIQVYEGGERAKTKDNNLGRPELSSIPAPKGVPOIEVTFDI 480
DB 421 PTKOTQLETTYSDNQPCVLLIQVYEGGERAKTKDNNLGRPELSSIPAPKGVPOIEVTFDI 480
QY 481 DANGIINVTATDSTGKANKITTTNDKGRLSKEIEEMVQAEKRYAEDVQERVSANK 540
DB 481 DANGIINVTATDSTGKANKITTTNDKGRLSKEIEEMVQAEKRYAEDVQERVSANK 540
QY 541 ALESYAFNMKSAVEDEGLKGISEADKKVLDKCOEYISWLDANTLAEKDEFHKKRELE 600
DB 541 ALESYAFNMKSAVEDEGLKGISEADKKVLDKCOEYISWLDANTLAEKDEFHKKRELE 600
QY 601 QVCNPIISGLYOGAGGPGFPGAQGPKGSGSGSPRTIEVD 641
DB 601 QVCNPIISGLYOGAGGPGFPGAQGPKGSGSGSPRTIEVD 641

```

```

RESULT 5
AAB23653
ID AAB23653 standard; protein; 640 AA.
XX
XX AAB23653:
AC
XX
XX 05-JAN-2001 (first entry)
DT
XX
XX
XX
XX

```

Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.

```

DE ATPase; Hsp70: heat shock protein; cytotoxic T lymphocyte; CTL;
KW immune response; infectious disease; malaria; cytotoxic T cell;
KW cytostatic; immunostimulant; cellular immune response inducer;
XX protozoicide; leukemia; cancer.
XX
XX Homo sapiens.
XX
XX WO200049041-A1.
XX
XX 24-AUG-2000.
XX
XX 18-FEB-2000; 2000WO-JP00941.
XX
XX 19-FEB-1999; 99JP-0041535.
XX
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX
XX Shinbara N, Udono H, Yui K;
XX
XX WPI; 2000-543748/49.
XX
XX Fused protein capable of inducing cellular immune response, useful as
PT active ingredient for drug compositions in preventing and/or treating
PT infectious diseases such as malaria or cancer -
XX
XX Claim 3; Page 49-52; 72pp; Japanese.
XX

```

The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and

CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.

XX Sequence 640 AA;

Query Match 99.4%; Score 3242.5; DB 21; Length 640;  
 Best Local Similarity 99.5%; Pred. No. 4e-223;  
 Matches 638; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNQYA 60  
 DB 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNQYA 60  
 QY 61 LNPQTVFDKRLIGRKFGDPVQSDMKHMPQVINDGDKPRVQSYSGETKAFPEETS 120  
 DB 61 LNPQTVFDKRLIGRKFGDPVQSDMKHMPQVINDGDKPRVQSYSGETKAFPEETS 120  
 QY 121 SMVLTKMEIAEAYLGYPVTAIVTPAYFNDQSOATKADAGVLAGLVLRITINEPTAA 180  
 DB 121 SMVLTKMEIAEAYLGYPVTAIVTPAYFNDQSOATKADAGVLAGLVLRITINEPTAA 180  
 QY 181 IAYGLDRGKGERNVLIIDLGSGTFDVSILITIDGIFEVKATAGDTHLGEDFDNRNVN 240  
 DB 181 IAYGLDRGKGERNVLIIDLGSGTFDVSILITIDGIFEVKATAGDTHLGEDFDNRNVN 240  
 QY 241 FVEEERKRRKKDISONKRAVRRLTACERAKRTLSSTQASLEISLPEGIDFYSTR 300  
 DB 241 FVEEERKRRKKDISONKRAVRRLTACERAKRTLSSTQASLEISLPEGIDFYSTR 300  
 QY 301 RPEELCSDFRSTLEPVEKALDKAQIHDVLVVGSGSTRIPRYOKLLDFFNGRDIN 360  
 DB 301 RPEELCSDFRSTLEPVEKALDKAQIHDVLVVGSGSTRIPRYOKLLDFFNGRDIN 360  
 QY 361 KSINDEAVAYGAAYQAAIILMGDKSENVDLLLDVAPLSLGLTAGGVMALIKRNSTI 420  
 DB 361 KSINDEAVAYGAAYQAAIILMGDKSENVDLLLDVAPLSLGLTAGGVMALIKRNSTI 420  
 QY 421 PTKQOIFTTYSNDQPGVLIQYBEGERAMTKDNLLGRFELSGLPPARGVQIETVPI 480  
 DB 421 PTKQOIFTTYSNDQPGVLIQYBEGERAMTKDNLLGRFELSGLPPARGVQIETVPI 480  
 QY 481 DANGILNTATDKSTGKANKITITNDKGRLSKEEIERMVAQEAKEYKADEVOREVSAKN 540  
 DB 481 DANGILNTATDKSTGKANKITITNDKGRLSKEEIERMVAQEAKEYKADEVOREVSAKN 540  
 QY 541 ALESYAFNMKSAVEDEGLKGTISEADKKKVLDKCOEVIISWLDANTLAEKDEFEHRRKELE 600  
 DB 541 ALESYAFNMKSAVEDEGLKGTISEADKKKVLDKCOEVIISWLDANTLAEKDEFEHRRKELE 600  
 QY 601 QVCNPIISGLYQAGPGCGFAGAGPKGSGSGPTIEVD 641  
 DB 600 QVCNPIISGLYQAGPGCGFAGAGPKGSGSGPTIEVD 640

RESULT 6  
 AAM10065  
 ID AAM10065 standard; Protein; 640 AA.

XX AAM10065;

XX 24-OCT-1997 (first entry)

XX Human heat shock protein 70.

XX Human heat shock protein 70; HSP70; primer: probe: detection;

XX intracellular; abnormal transcription; acute; chronic; sustained;

XX stress.

XX Homo sapiens.

XX JP08322577-A.  
 XX 10-DEC-1996.  
 XX 01-JUN-1995; 95JP-0158581.  
 XX 01-JUN-1995; 95JP-0158581.  
 XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX WPI: 1997-081088/08.  
 XX N-PSDB: AAT58086.  
 DR Detection of abnormal transcription of HSP70 mRNA - using HSP70  
 XX specific primer or probe, used in detection of human acute and  
 XX chronic sustained stress load  
 PS Claim 1; Fig 1; 13pp; Japanese.  
 CC The cDNA encoding the present sequence, human heat shock protein 70  
 CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
 CC and 21. Primers and probes based on the HSP70 cDNA coding  
 CC sequence can be used to detect the abnormal transcription of  
 CC intracellular HSP70 mRNA in human acute and chronic sustained  
 CC stress load.

XX Sequence 640 AA;

Query Match 99.0%; Score 3229.5; DB 18; Length 640;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-222;  
 Matches 636; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNQYA 60  
 DB 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNQYA 60  
 QY 61 LNPQTVFDKRLIGRKFGDPVQSDMKHMPQVINDGDKPRVQSYSGETKAFPEETS 120  
 DB 61 LNPQTVFDKRLIGRKFGDPVQSDMKHMPQVINDGDKPRVQSYSGETKAFPEETS 120  
 QY 121 SMVLTKMEIAEAYLGYPVTAIVTPAYFNDQSOATKADAGVLAGLVLRITINEPTAA 180  
 DB 121 SMVLTKMEIAEAYLGYPVTAIVTPAYFNDQSOATKADAGVLAGLVLRITINEPTAA 180  
 QY 181 IAYGLDRGKGERNVLIIDLGSGTFDVSILITIDGIFEVKATAGDTHLGEDFDNRNVN 240  
 DB 181 IAYGLDRGKGERNVLIIDLGSGTFDVSILITIDGIFEVKATAGDTHLGEDFDNRNVN 240  
 QY 241 FVEEERKRRKKDISONKRAVRRLTACERAKRTLSSTQASLEISLPEGIDFYSTR 300  
 DB 241 FVEEERKRRKKDISONKRAVRRLTACERAKRTLSSTQASLEISLPEGIDFYSTR 300  
 QY 301 RPEELCSDFRSTLEPVEKALDKAQIHDVLVVGSGSTRIPRYOKLLDFFNGRDIN 360  
 DB 301 RPEELCSDFRSTLEPVEKALDKAQIHDVLVVGSGSTRIPRYOKLLDFFNGRDIN 360  
 QY 361 KSINDEAVAYGAAYQAAIILMGDKSENVDLLLDVAPLSLGLTAGGVMALIKRNSTI 420  
 DB 361 KSINDEAVAYGAAYQAAIILMGDKSENVDLLLDVAPLSLGLTAGGVMALIKRNSTI 420  
 QY 421 PTKQOIFTTYSNDQPGVLIQYBEGERAMTKDNLLGRFELSGLPPARGVQIETVPI 480  
 DB 421 PTKQOIFTTYSNDQPGVLIQYBEGERAMTKDNLLGRFELSGLPPARGVQIETVPI 480  
 QY 481 DANGILNTATDKSTGKANKITITNDKGRLSKEEIERMVAQEAKEYKADEVOREVSAKN 540  
 DB 481 DANGILNTATDKSTGKANKITITNDKGRLSKEEIERMVAQEAKEYKADEVOREVSAKN 540  
 QY 541 ALESYAFNMKSAVEDEGLKGTISEADKKKVLDKCOEVIISWLDANTLAEKDEFEHRRKELE 600  
 DB 541 ALESYAFNMKSAVEDEGLKGTISEADKKKVLDKCOEVIISWLDANTLAEKDEFEHRRKELE 600

QY 601 QVCNPIISGLYOGAGPGPGFGAOGPKGGSGSGPTIEVD 641  
 Db 600 QVCNPIISGLYOGAGPGPGFGAOGPKGGSGSGPTIEVD 640

# RESULT 7

AAV88408  
 ID AAV88408 standard; Protein; 640 AA.

XX AAV88408;

XX 31-JUL-2000 (first entry)

XX Human heat shock protein HSP70 amino acid sequence.

XX Human: heat shock protein: HSP70; chromosome 6p21.3-22; stress:

KM chromosome 14q22-24; transcription; rheumatism; schizophrenia;

XX depression; nephrotic syndrome.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

XX N-PSDB; AAA15620.

XX Abnormal transcription of intracellular HSP70mRNA under acute and

PT chronic continuous load of stress in a human being and its application

XX Claim 2; Fig 1; 11pp; Japanese.

XX This sequence represents the human heat shock protein HSP70 amino acid

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22

CC and 14q22-24. The invention relates to the abnormal transcription of

CC intracellular HSP70mRNA under acute and chronic stress load in a human.

CC The abnormal transcription of HSP70 can be used in the improvement of

CC stress and response and diagnosis of stress diseases including

CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 640 AA;

XX Query Match 99.0%; Score 3229.5; DB 21; Length 640;

XX Best Local Similarity 99.2%; Pred. No. 3.4e-222;

XX Matches 636; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MAKAAAGIDGTTTSCVGFQHGKVEIANDGNNRTTPTSYVAFDTRERLIGDAKNOVA 60

Db 1 MAKAAAGIDGTTTSCVGFQHGKVEIANDGNNRTTPTSYVAFDTRERLIGDAKNOVA 60

QY 61 LNPONTYFDKRLIGRFGDPVQSDMKHMPQVYINDGDKPKVQSYKGETKATYPEIS 120

Db 61 LNPONTYFDKRLIGRFGDPVQSDMKHMPQVYINDGDKPKVQSYKGETKATYPEIS 120

QY 121 SMVTKKKEIAEAYLGPVNAVTVPAYFNDOSORATKAGVAGNLVRLINEPTAAA 180

Db 121 SMVTKKKEIAEAYLGPVNAVTVPAYFNDOSORATKAGVAGNLVRLINEPTAAA 180

QY 181 IAVGLDRTGGERNVLLFDLGGGTFDVSILITIDGIEVATAGDTHLGGEDFENRLVNH 240

Db 181 IAVGLDRTGGERNVLLFDLGGGTFDVSILITIDGIEVATAGDTHLGGEDFENRLVNH 240

QY 241 FVEEFKKHKKDISQNRRAVRRLTACERAKRLSSSTQASLEIDSLFEGIDFTYSTR 300

Db 241 FVEEFKKHKKDISQNRRAVRRLTACERAKRLSSSTQASLEIDSLFEGIDFTYSTR 300

QY 301 RFEEICSDLFRSTLEPEYERAKLRDAKIDKAOIHDLVYVGGSTRIPKYOQLQDFENGNDLN 360  
 Db 301 RFEEICSDLFRSTLEPEYERAKLRDAKIDKAOIHDLVYVGGSTRIPKYOQLQDFENGNDLN 360  
 QY 361 KSINPDEAVAYGAQVAAIIMGDKSENVODLLIDVAPLSLGETAGVWTFALIKRNTI 420  
 Db 361 KSINPDEAVAYGAQVAAIIMGDKSENVODLLIDVAPLSLGETAGVWTFALIKRNTI 420  
 QY 421 PTKOTOFETTSNQPVLQVYEGGERAMTKDNNLGRFELSGIPAPRGVPOIEVTFDI 480  
 Db 421 PTKOTOFETTSNQPVLQVYEGGERAMTKDNNLGRFELSGIPAPRGVPOIEVTFDI 479  
 QY 481 DANGILNVTATDKSTGKANKITITNDKGRLSKEIEIRMYOEAERYAEDVEQREVSANK 540  
 Db 480 DANGILNVTATDKSTGKANKITITNDKGRLSKEIEIRMYOEAERYAEDVEQREVSANK 539  
 QY 541 ALESYAFNMKSAYVEDEGLKRISEADKKVLDKCOEYISWLDANTLAEKDFEKKRELE 600  
 Db 540 ALESYAFNMKSAYVEDEGLKRISEADKKVLDKCOEYISWLDANTLAEKDFEKKRELE 599  
 QY 601 QVCNPIISGLYOGAGPGPGFGAOGPKGGSGSGPTIEVD 641  
 Db 600 QVCNPIISGLYOGAGPGPGFGAOGPKGGSGSGPTIEVD 640

## RESULT 8

AAAR03929  
 ID AAR03929 standard; Protein; 640 AA.

XX AAR03929;

XX 30-AUG-1990 (first entry)

XX Homo sapiens HSP (humhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Homo sapiens.

XX Key Location/Qualifiers

FT MISC-difference 640 /note="residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODON-) CODON.

XX Dragon E; Faulds D; Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used

PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has

CC 641 amino acid residues, the sequence itself has only 640,

CC including "O" (?) at position 640.

CC Fig. 2 provides an alignment of heat shock proteins from a variety

CC of organisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03922);

CC 2. Bacillus megaterium (Bmebsp70 - AAR03923);

CC 3. E. coli (dnak - AAR03924);

CC 4. T. cruzi (tcr70kd - AAR03925);

CC 5. T. cruzi (AAR03926);

CC 6. Rat rattus (rathsp70 - AAR03927);

```

CC 7. Xenopus laevis (x170 - AAR03928);
CC 8. Homo sapiens (humbsp70 - AAR03929);
CC 9. Gallus gallus (chhbsp70 - AAR03930);
CC 10. Zea mays (mzensp70 - AAR03931);
CC 11. Serattia marcescens (smasp70 - AAR03932).
CC The proteins having homology to hsp's of T. cruzi can be used in
CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
CC Mycobacteria species.
XX
SQ Sequence 640 AA;

Query Match 98.4%; Score 3211; DB 11; Length 640;
Best Local Similarity 98.9%; Pred. No. 7.2e-221;
Matches 634; Conservative 2; Mismatches 3; Indels 2; Gaps 2;

QY 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAAKNOVA 60
DB 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAAKNOVA 60
QY 61 LNPQNTVFDAKRLIGRKGDPPVQSDMKHMPVOYINDGDKPKVOYSGYGETKAFPEEIS 120
DB 61 LNPQNTVFDAKRLIGRKGDPPVQSDMKHMPVOYINDGDKPKVOYSGYGETKAFPEEIS 120
QY 121 SMVLTKMKEIAEAYLYGYEVTNAVITVPAYFNDQSOQATKDAAGVIALVLRITINEPTAAA 180
DB 121 SMVLTKMKEIAEAYLYGYEVTNAVITVPAYFNDQSOQATKDAAGVIALVLRITINEPTAAA 180
QY 181 IAYGLDRTGKGERNVLIFFDLGGTFDVSILITDDGIFEVKAATAGDTHLGEDFDNRNLVNH 240
DB 181 IAYGLDRTGKGERNVLIFFDLGGTFDVSILITDDGIFEVKAATAGDTHLGEDFDNRNLVNH 240
QY 241 FVEEFKRKHKKDISONKRAVRRLTACERAKRTLSSTQASLEIDSLPEGIDFVYSITRA 300
DB 241 FVEEFKRKHKKDISONKRAVRRLTACERAKRTLSSTQASLEIDSLPEGIDFVYSITRA 300
QY 301 RFEELCSDFRSTLEPYEKALRDAKLDKAQIHDVLVVGSGSTRIPVQKLLDFFNGRDLN 360
DB 301 RFEELCSDFRSTLEPYEKALRDAKLDKAQIHDVLVVGSGSTRIPVQKLLDFFNGRDLN 360
QY 361 KSINPDEVAVGAOVAQAAIIMGDKSENVODLLDLVAPLSIGLETFAGGVMTALIKRNSTI 420
DB 361 KSINPDEVAVGAOVAQAAIIMGDKSENVODLLDLVAPLSIGLETFAGGVMTALIKRNSTI 420
QY 421 PTKQTOITTTSDNOPGVLIQYEGERAMTKDNMLGRFELSGIPPARGVQIETVETDI 480
DB 421 PTKQTOITTTSDNOPGVLIQYEGERAMTKDNMLGRFELSGIPPARGVQIETVETDI 480
QY 481 DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVOEAEKKYKADEVQREKVSAN 540
DB 481 DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVOEAEKKYKADEVQREKVSAN 540
QY 541 ALESTAFPMKSAVEDEGLKGIKISEADKKVLDKCOEVIISWLDANTLAEKDEFEHRRKELE 600
DB 541 ALESTAFPMKSAVEDEGLKGIKISEADKKVLDKCOEVIISWLDANTLAEKDEFEHRRKELE 600
QY 601 QVCNPIISGLVQAGGPGGFGAGCPKGGSGSGPTIEVD 641
DB 601 QVCNPIISGLVQAGGPGGFGAGCPKGGSGSGPTIEVD 641

RESULT 9
AAB23252 ID AAB23252 standard; Protein: 624 AA.
AC AAB23252;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human Hsp72 (heat shock protein 72).
DE
XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
KW expression modulator; JNK phosphatase inhibitor; antiproliferative;
KW drug screening; cancer; leukemia; Lymphoma; solid tumour; sarcoma.

```

```

KW carcinoma; breast cancer; prostate cancer; premalignant condition.
XX
XX Homo sapiens.
OS
XX WO200054814-A1.
XX
XX 21-SEP-2000.
PD
XX 17-MAR-2000; 2000WO-US07350.
PE
XX 18-MAR-1999; 99US-0125046.
PR
XX (PHYL-) PHYLOGENY INC.
PA
XX Volloch VZ, Sherman M;
PI
XX WPI: 2000-647056/62.
DR
XX N-PSDB: AAA97541.
XX
XX Identifying compounds that inhibit proliferation of cells and capable
PT of modulating the expression of heat shock protein 72 gene and/or
PT activity of Hsp72 useful for treating cancers such as leukemia,
PT lymphoma
XX
XX Examples: Fig 16b; 77pp; English.
XX
XX The invention relates to a novel method of identifying compounds that
CC inhibit proliferation of cells comprising contacting a test compound with
CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining
CC if the test compound inhibits activity or expression of Hsp72.
CC Optionally, Hsp72 is contacted with the test compound under optimum
CC conditions to allow the two components to interact and bind, forming a
CC complex which is detected. The invention also relates to a method of
CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase
CC activation, comprising contacting a test compound with a cell which
CC expresses Hsp72, exposing the cell to a heat induced stress and
CC determining if the compound inhibits JNK phosphatase activity. The
CC invention additionally encompasses compositions comprising an inhibitor
CC of Hsp72 or JNK phosphatase activity. The compounds identified as
CC inhibitors of Hsp72 or JNK phosphatase activity are useful for
CC inhibiting the proliferation of cells. Modulation of the activity of the
CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such
CC as cancers (e.g., leukemia, lymphoma, solid tumours such as sarcomas and
CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit
CC Hsp72 activity can also be administered to treat premalignant conditions
CC and to prevent progression to a neoplastic or malignant state. The
CC compounds that inhibit Hsp72 function are administered to a patient
CC having a disease or disorder mediated by an increase of Hsp72 expression
CC or activity relative to normal levels. The present sequence represents
CC human Hsp72 used in the exemplifications of the invention.
XX
SQ Sequence 624 AA;

Query Match 97.2%; Score 3172; DB 21; Length 624;
Best Local Similarity 100.0%; Pred. No. 4.2e-218;
Matches 624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAAKNOVA 60
DB 1 MAKAAAGIDIGTYSVGVFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAAKNOVA 60
QY 61 LNPQNTVFDAKRLIGRKGDPPVQSDMKHMPVOYINDGDKPKVOYSGYGETKAFPEEIS 120
DB 61 LNPQNTVFDAKRLIGRKGDPPVQSDMKHMPVOYINDGDKPKVOYSGYGETKAFPEEIS 120
QY 121 SMVLTKMKEIAEAYLYGYEVTNAVITVPAYFNDQSOQATKDAAGVIALVLRITINEPTAAA 180
DB 121 SMVLTKMKEIAEAYLYGYEVTNAVITVPAYFNDQSOQATKDAAGVIALVLRITINEPTAAA 180
QY 181 IAYGLDRTGKGERNVLIFFDLGGTFDVSILITDDGIFEVKAATAGDTHLGEDFDNRNLVNH 240
DB 181 IAYGLDRTGKGERNVLIFFDLGGTFDVSILITDDGIFEVKAATAGDTHLGEDFDNRNLVNH 240

```

```

QY 241 FVEEFKRRKKKDISQNKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYTSITRA 300
    |||
DB 241 FVEEFKRRKKKDISQNKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYTSITRA 300
QY 301 REEELCSDLFRSTLPEVEKALRDADKQIHDLVVGSGSTRPKYOKLLODFPNRDLN 360
    |||
DB 301 REEELCSDLFRSTLPEVEKALRDADKQIHDLVVGSGSTRPKYOKLLODFPNRDLN 360
QY 361 KSINPDEAVAYGAAYOAAIIMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420
    |||
DB 361 KSINPDEAVAYGAAYOAAIIMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420
QY 421 PTKOTQITFTTYSNQPGLVLYQYEGERAMTKDNNLLGREELSGIPAPRGVPOIEVTFDI 480
    |||
DB 421 PTKOTQITFTTYSNQPGLVLYQYEGERAMTKDNNLLGREELSGIPAPRGVPOIEVTFDI 480
QY 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEIERMVOEAKRYAEDVOERVSAN 540
    |||
DB 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEIERMVOEAKRYAEDVOERVSAN 540
QY 541 ALESYAFNMKSAVEDGLKGISEADKKVLDKQCEYISWLDANTLAERKDEFEHKKRELE 600
    |||
DB 541 ALESYAFNMKSAVEDGLKGISEADKKVLDKQCEYISWLDANTLAERKDEFEHKKRELE 600
QY 601 QVCNPIISGLYOGAGGPGPGFGA 624
    |||
DB 601 QVCNPIISGLYOGAGGPGPGFGA 624

```

RESULT 10  
ID AAR43004  
AAR43004 standard; protein; 641 AA.

AC AAR43004;

XX 20-MAY-1994 (first entry)

DE Mature mouse sperm 70KD heat shock protein.

XX Sulphoglycolipid immobilising protein 1; sperm plasma membrane;

KW HSC70B; mammalian; infertility; mycoplasma; HSP70.

XX Mus musculus.

XX Key  
FH Region

Location/Qualifiers  
1..385

/label= 44kD\_Atpase\_fragment

/note= "peptides comprising an intact domain from

the Atpase fragment of hsp70 are claimed;

the peptides are homologous to sequences

conserved between Stip1 and 74.5kD

mycoplasma protein"

1..39

/label= IA

/note= "part"

40..115

/label= IB

116..188

/label= IA

/note= "part"

189..228

/label= IIA

/note= "part"

229..306

/label= IIB

307..385

/label= IIA

/note= "part"

Domain

Domain

Domain

Domain

Domain

Domain

Domain

XX MO9321954-A.

XX 11-NOV-1993.

XX

XX

XX

XX

PF 22-APR-1993; 93WO-US03816.

XX

PR 24-APR-1992; 92US-0873961.

XX

PA (BERL-) BERLEX LAB INC.

XX (OTTR-) OTTAWA CIVIC HOSPITAL.

XX

PI Pauls DH, Lingwood CA, Tanphalchitr N;

XX WPI; 1993-368422/46.

DR

XX

PT Mammalian fertilisation decrease for detecting and treating

XX infertility - using sulpo glyco lipid immobilising protein

PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma

XX infection treatment

PS Claim 2 and Claim 17; Page 60-62; 77pp; English.

XX

XX

CC The likelihood of mammalian fertilisation is decreased by contacting

CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/

CC sulphated glyco-moiety interfering composition. The interfering

CC compsn. is e.g. the heat shock 70KD protein, Stip1 (or analogues

CC such as the mouse Stip1 analogue "HSC70B" comprising the amino acid

CC sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).

XX

SQ Sequence 641 AA;

Query Match 95.9%; Score 3130; DB 14; Length 641;

Best Local Similarity 95.2%; Pred. No. 4.4e-215;

Matches 610; Conservative 20; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAKAAAGIDLGTTYSQVGFQHGKVEIANDQGNFTTFSYAFDTERTLIGDAKNQYA 60

DB 1 MAKNTAIGIDLGTTYSQVGFQHGKVEIANDQGNFTTFSYAFDTERTLIGDAKNQYA 60

QY 61 LNPONTVFDAKRLIGKFGDPVVOQSDMKHMPVOYINDGDKPKYOVSYKSETAFYEIS 120

DB 61 LNPONTVFDAKRLIGKFGDPVVOQSDMKHMPVOYINDGDKPKYOVSYKSETAFYEIS 120

QY 121 SWVLTKMKELAEAYLGYPYNAVITYPAYFNDSORATDAGYIACLVNLRITNEPTAA 180

DB 121 SWVLTKMKELAEAYLGYPYNAVITYPAYFNDSORATDAGYIACLVNLRITNEPTAA 180

QY 121 IAYGLDRTGGERNVLIIFDGGGTFDVSILYIDDGIFEVKATAGDTHLGGEFDNRLVN 240

DB 181 IAYGLDRTGGERNVLIIFDGGGTFDVSILYIDDGIFEVKATAGDTHLGGEFDNRLVN 240

QY 241 FVEEFKRRKKDISQNKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYTSITRA 300

DB 241 FVEEFKRRKKDISQNKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFTYTSITRA 300

QY 301 RPEELCSDLFRSTLPEVEKALRDADKQIHDLVVGSGSTRPKYOKLLODFPNRDLN 360

DB 301 RPEELCSDLFRSTLPEVEKALRDADKQIHDLVVGSGSTRPKYOKLLODFPNRDLN 360

QY 361 KSINPDEAVAYGAAYOAAIIMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420

DB 361 KSINPDEAVAYGAAYOAAIIMGDKSENVODLLLDVAPLSLGETAGVMTALIKRNSTI 420

QY 421 PTKOTQITFTTYSNQPGLVLYQYEGERAMTKDNNLLGREELSGIPAPRGVPOIEVTFDI 480

DB 421 PTKOTQITFTTYSNQPGLVLYQYEGERAMTKDNNLLGREELSGIPAPRGVPOIEVTFDI 480

QY 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEIERMVOEAKRYAEDVOERVSAN 540

DB 481 DANGILNVTATDKSTGKANKITTTNDKGRLSKEIERMVOEAKRYAEDVOERVSAN 540

QY 541 ALESYAFNMKSAVEDGLKGISEADKKVLDKQCEYISWLDANTLAERKDEFEHKKRELE 600

DB 541 ALESYAFNMKSAVEDGLKGISEADKKVLDKQCEYISWLDANTLAERKDEFEHKKRELE 600

QY 601 QVCNPIISGLYOGAGGPGPGFGA 624

DB 601 QVCNPIISGLYOGAGGPGPGFGA 624

Db 601 RVCSPITISGLYOGAGAPGAGFGAOPKAGSGSGPTIEVD 641

RESULT 11

AAB23650

ID AAB23650 standard; protein: 642 AA.

XX

AC AAB23650;

XX

XX 05-JAN-2001 (first entry)

DE Rat heat shock protein Hsp70.1 protein sequence SEQ ID NO:2.

XX

XX

KW Atpase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;

KW immune response; infectious disease; malaria; cytotoxic T cell;

KW cytosolic; immunostimulant; cellular immune response inducer;

KW protozoacide; leukemia; cancer.

XX

OS Rattus sp.

XX

PN MO200049041-A1.

XX

PD 24-AUG-2000.

XX

PF 18-FEB-2000; 2000MO-JP00941.

XX

PR 19-FEB-1999; 99JP-0041535.

XX

PA (SOME ) SUMITOMO ELECTRIC IND CO.

XX

PI Shinbara N, Uono H, Yui K;

XX

DR WPI; 2000-543748/49.

XX

PT Fused protein capable of inducing cellular immune response, useful as

PT active ingredient for drug compositions in preventing and/or treating

PT infectious diseases such as malaria or cancer

XX

PS Claim 3; Page 39-42; 72pp; Japanese.

XX

CC The present invention describes a fused protein (1) prepared from a

CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by

CC cytotoxic T cells and a protein containing the Atpase domain of a heat

CC shock protein. Also described are: (1) a drug composition containing (1)

CC as active ingredient; (2) a DNA encoding (1); (3) an expression vector

CC containing the DNA of (2); and (4) a transformant which can retain the

CC expression vector of (3). (1) has cytosolic, immunostimulant and

CC protozoacide activities, and can be used as a cellular immune response

CC inducer. The protein is useful as an active ingredient for drug

CC compositions in preventing and/or treating infectious diseases such as

CC malaria or cancer e.g. to provide systemic immunity against leukaemia.

CC The present sequence represents a specifically claimed heat shock

CC protein for use in a fused protein of the present invention.

XX

SO Sequence 642 AA;

Query Match 95.88; Score 3125.5; DB 21; Length 642;

Best Local Similarity 95.28; Pred. No. 9.2e-215;

Matches 611; Conservative 20; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAKAAAGIDIDGTTYSQGVFQHGKVELIANDQGNRTPSVAFTDRLTGDAKNQVA 60

DB 1 MAKMTAIGIDIDGTTYSQGVFQHGKVELIANDQGNRTTPSVAFDTRLTGDAKNQVA 60

QY 61 LNPQNTVFDAKRLIGRKFGDEPVOSDMKMPFOVINDGDKPVQSYSGETKAFYPERIS 120

DB 61 LNPQNTVFDAKRLIGRKFGDAVQSDMKMPFOVINDGDKRVQNYNGESRFFPERIS 120

QY 121 SMVLTKKKEIAEAYLGIPYTNAAVITPAVYFNDQKATKAGVAGLNLVRLINEPTAA 180

DB 121 SMVLTKKKEIAEAYLGIPYTNAAVITPAVYFNDQKATKAGVAGLNLVRLINEPTAA 180

QY 181 IAYGLDRFGKGERNVLIJFDLGSGTFDVSILTIIDGIFEVKATAGDTHLGDEFDRLNVH 240

Db 181 IAYGLDRFGKGERNVLIJFDLGSGTFDVSILTIIDGIFEVKATAGDTHLGDEFDRLNVH 240

QY 241 FVEEFKRRKKRDISONKRAVRRLTACERAKRTSSSTQASLEIDSLFEGIDFTYSTR 300

DB 241 FVEEFKRRKKRDISONKRAVRRLTACERAKRTSSSTQASLEIDSLFEGIDFTYSTR 300

QY 301 RFEELCSDLEFRGTLEPVKALRDAMDKAOJHDLVLVGGSTRIPVQKLQDFNGRDLN 360

DB 301 RFEELCSDLEFRGTLEPVKALRDAMDKAOJHDLVLVGGSTRIPVQKLQDFNGRDLN 360

QY 361 KSINPDEAVAGAAVOAAIILMGDKSENQDILLIDVAPLSGLETAGSVMTALIKRNTI 420

DB 361 KSINPDEAVAGAAVOAAIILMGDKSENQDILLIDVAPLSGLETAGSVMTALIKRNTI 420

QY 421 PTKOTQITFTYSDNPGVLIQVYBGERAMTYDNLLRFEELSGIPAPRAGVPQLEVF 480

DB 421 PTKOTQITFTYSDNPGVLIQVYBGERAMTYDNLLRFEELSGIPAPRAGVPQLEVF 480

QY 481 DANGILNTATDQSKGANKITITNDKGRLSKEELERWQAEKKADEVOERVSAN 540

DB 481 DANGILNTATDQSKGANKITITNDKGRLSKEELERWQAEKKADEVOERVSAN 540

QY 541 ALESYAFNMKSAVEDEGLKGRKISEADKKVLDKQCEVISMIDANTLAEKDFEHRKKE 600

DB 541 ALESYAFNMKSAVEDEGLKGRKISEADKKVLDKQCEVISMIDANTLAEKDFEHRKKE 600

QY 601 QVCNPIISGLYOGAGPGPGFGAOG-PKSGSGSGPTIEVD 641

DB 601 RVCSPITISGLYOGAGAPGAGFGAOPKAGSGSGPTIEVD 642

RESULT 12

AAY88411

ID AAY88411 standard; Protein: 640 AA.

XX

AC AAY88411;

XX

XX 31-JUL-2000 (first entry)

XX

DE Human heat shock protein LHSPT70 amino acid sequence.

XX

XX

KW Human: heat shock protein; HSP70; chromosome 6p21.3-22; stress;

KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;

XX

OS Homo sapiens.

XX

PN JP2000069999-A.

XX

PD 07-MAR-2000.

XX

PF 01-JUN-1995; 99JP-0257146.

XX

PR 01-JUN-1995; 95JP-0158581.

XX

PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX

DR WPI; 2000-264458/23.

XX

PT Abnormal transcription of intracellular HSP70mRNA under acute and

PT chronic continuous load of stress in a human being and its application

XX

PS Disclosure; Fig 4; 11pp; Japanese.

XX

CC This sequence represents the human heat shock protein LHSPT70 amino acid

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22

CC and 14q22-24. The invention relates to the abnormal transcription of

CC intracellular HSP70mRNA under acute and chronic stress load in a human.

CC The abnormal transcription of HSP70 can be used in the improvement of

CC stress and response and diagnosis of stress diseases including

CC rheumatism, schizophrenia, depression and nephrotic syndrome.







CC can be detected using 2D gel electrophoresis comparison of cell lysates.  
CC The proteins can be used as biochemical markers to detect the phase of  
CC the endometrium and can be measured in body fluids, obviating the need  
CC for endometrial biopsies.

XX  
SQ Sequence 646 AA:

Query Match 87.6%; Score 2859.5; DB 19; Length 646;  
Best Local Similarity 85.6%; Pred. No. 9.3e-196;  
Matches 553; Conservative 48; Mismatches 40; Indels 5; Gaps 3;

```
QY 1 MAKAAIGIDLTGTTSCVGFQHGKVEITANDGNRTTSPSYAFDTERLIGDAKNOVA 60
    1 MSKGPAYGIDLTGTTSCVGFQHGKVEITANDGNRTTSPSYAFDTERLIGDAKNOVA 60
Db 1 MSKGPAYGIDLTGTTSCVGFQHGKVEITANDGNRTTSPSYAFDTERLIGDAKNOVA 60
QY 61 LNPONTVPFAKRLIGKRFDPVQSDMKHMPFQVINDGDKPKVOVSKGFTAKFPEEIS 120
    61 MNPNTVPFAKRLIGKRFDPDVAVQSDMKHMPFQVINDAGPKVOVEYKGETSFPEEVS 120
Db 61 MNPNTVPFAKRLIGKRFDPDVAVQSDMKHMPFQVINDAGPKVOVEYKGETSFPEEVS 120
QY 121 SMVLTMKKEIAEAYLGYPTNAVITVPAYFNSQROATKDAGYIAGIANYLRIINEPTAA 180
    121 SMVLTMKKEIAEAYLGKTYNNAVITVPAYFNSQROATKDAGTIAGIANYLRIINEPTAA 180
Db 121 SMVLTMKKEIAEAYLGKTYNNAVITVPAYFNSQROATKDAGTIAGIANYLRIINEPTAA 180
QY 181 IAVGLDRFGKGERNVLIIFDLGGGTFDVSILTIIDGIFEVKATAGDTHLGGEDEFNRLVNH 240
    181 IAVGLDRKKGAEERNVLIIFDLGGGTFDVSILTIIDGIFEVKSTAGDTHLGGEDEFNRMVNH 240
Db 181 IAVGLDRKKGAEERNVLIIFDLGGGTFDVSILTIIDGIFEVKSTAGDTHLGGEDEFNRMVNH 240
QY 241 FVVEEFRRKKKDIOSOKRAVRRLRTACERAKRLSSQASLEIDSLFEGIDPFTSITRA 300
    241 FIAEFRRKKKDIOSOKRAVRRLRTACERAKRLSSQASLEIDSLYEGIDPFTSITRA 300
Db 241 FIAEFRRKKKDIOSOKRAVRRLRTACERAKRLSSQASLEIDSLYEGIDPFTSITRA 300
QY 301 REEELCSDFRSTLEPVERAKLRDAKLDKAOIHDVLVVGSTRIIPKYOKLIDPFNGRDIN 360
    301 REEELNADLFPGTLDPEKALRDAKLDKQIHDVLVVGSTRIIPKIQKLLQDFENGKEIN 360
Db 301 REEELNADLFPGTLDPEKALRDAKLDKQIHDVLVVGSTRIIPKIQKLLQDFENGKEIN 360
QY 361 KSIINPEAVAYGAOAAIIMGDKSENVODLLIDVAPLSLGLTAGVWTALIKRNTI 420
    361 KSIINPEAAVAYGAOAAIISGDKSENVODLLLDVYPLSLGIEIAGVWTALIKRNTI 420
Db 361 KSIINPEAAVAYGAOAAIISGDKSENVODLLLDVYPLSLGIEIAGVWTALIKRNTI 420
QY 421 PTRKQOIFTTTYSNPGVLIQVEGERAMTKDNNLIGREFLSGIRPAPRGVQIEVTFDI 480
    421 PTRKQOTFTTYSNPGVLIQVEGERAMTKDNNLIGKFEFTGIRPAPRGVQIEVTFDI 480
Db 421 PTRKQOTFTTYSNPGVLIQVEGERAMTKDNNLIGKFEFTGIRPAPRGVQIEVTFDI 480
QY 481 DANGILNVTATDSTGKANKITITNDKGRSLKEEIRMYQEAKEYKAEDDEVQREERYSAKN 540
    481 DANGILNVSAYDKSTGKANKITITNDKGRSLKEDIERMYQEAKEYKAEDDEKQORDYSSKN 540
Db 481 DANGILNVSAYDKSTGKANKITITNDKGRSLKEDIERMYQEAKEYKAEDDEKQORDYSSKN 540
QY 541 ALBSTYAFNMKSAVEDGLKGISADKKVLDKQCEVISMLDANTLAEKDEFEHKKRELE 600
    541 SLESTYAFNMKATVEDEKLGKINDEDKQILDCNEIIMWLDKQTAERKEEFEHQQELE 600
Db 541 SLESTYAFNMKATVEDEKLGKINDEDKQILDCNEIIMWLDKQTAERKEEFEHQQELE 600
QY 601 QVCNPIISGLYQAGG-PCG--PGGF--GAQGPKGSGSGSPTTIEVD 641
    601 KVCNPIITRLYQAGGPGGPGGAPPGGASGSPITIEVD 646
Db 601 KVCNPIITRLYQAGGPGGPGGAPPGGASGSPITIEVD 646
```

Search completed: December 4, 2002, 16:41:55  
Job time : 41 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:50:13 ; Search time 38 Seconds  
(without alignments)  
3475.689 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 641

Sequence: 1 MAKAAAGIDLGTTTSCVGV.....FGAGPGKSGSGPTIEVD 641

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.potent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	49.6	640	6 Q8WNS9	Q8WNS9 canis fam11
2	150	23.4	151	4 Q9UQC1	Q9UQC1 homo sapien
3	114	17.8	641	11 Q63256	Q63256 rattus norv
4	101	15.8	641	11 Q9OM75	Q9OM75 mus musculu
5	101	15.8	642	11 Q925V6	Q925V6 mus musculu
6	73	11.4	455	11 Q63718	Q63718 rattus rat
7	72	11.2	641	4 Q75634	Q75634 homo sapien
8	72	11.2	641	4 Q96OC9	Q96OC9 homo sapien
9	60	9.4	228	11 Q61698	Q61698 mus musculu
10	58	9.0	247	13 Q98896	Q98896 fugu rubrip
11	58	9.0	639	13 Q73922	Q73922 creochromis
12	58	9.0	639	13 Q8UM99	Q8UM99 xiphophorus
13	56	8.7	637	13 Q8UM98	Q8UM98 xiphophorus
14	55	8.6	111	11 Q9R2A1	Q9R2A1 mus musculu
15	55	8.6	633	11 Q99KD7	Q99KD7 mus musculu
16	55	8.6	636	6 Q9TUG3	Q9TUG3 capra hircu

17	55	8.6	641	11 Q88686	Q88686 mus musculu
18	55	8.6	644	5 Q95V47	Q95V47 artemia san
19	55	8.6	658	13 Q9TAC1	Q9TAC1 brachydanio
20	54	8.4	638	13 Q8UM90	Q8UM90 xiphophorus
21	54	8.4	640	13 Q93240	Q93240 paralichthy
22	54	8.4	644	13 Q8UM96	Q8UM96 oncorhynch
23	53	8.3	493	4 Q9H3K6	Q9H3K6 homo sapien
24	53	8.3	566	6 Q95LNG	Q95LNG macaca fasc
25	53	8.3	646	13 Q73885	Q73885 gallus gall
26	53	8.3	647	13 Q91993	Q91993 xenopus lae
27	53	8.3	651	5 Q8SX04	Q8SX04 drosophila
28	53	8.3	651	13 Q8UV14	Q8UV14 ambystoma m
29	53	8.3	653	5 Q94805	Q94805 trichoplusi
30	52	8.1	649	13 P79984	P79984 brachydanio
31	51	8.0	79	6 Q95JRO	Q95JRO equus cabal
32	49	7.6	247	13 Q98901	Q98901 fugu rubrip
33	49	7.6	367	13 Q98899	Q98899 fugu rubrip
34	49	7.6	646	5 Q01948	Q01948 trichinella
35	48	7.5	552	11 Q9OM71	Q9OM71 mus musculu
36	48	7.5	646	10 Q959N1	Q959N1 arabidopsis
37	47	7.3	643	6 Q9NIU2	Q9NIU2 saginus oe
38	47	7.3	650	5 Q9GPK0	Q9GPK0 heterodera
39	45	7.0	599	5 Q8WQ94	Q8WQ94 crassostrea
40	45	7.0	636	5 Q18474	Q18474 biomphalari
41	45	7.0	636	5 Q44343	Q44343 biomphalari
42	45	7.0	639	13 Q98900	Q98900 fugu rubrip
43	45	7.0	646	5 Q94614	Q94614 mesocostoid
44	45	7.0	659	5 Q9XZJ2	Q9XZJ2 crassostrea
45	45	7.0	665	5 Q24789	Q24789 echinococcu

## ALIGNMENTS

RESULT 1	ID	Q8WNS9	PRELIMINARY:	PRT:	640 AA.
AC	Q8WNS9:				
DT	01-MAR-2002 (TREMBLrel. 20, Created)				
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Heat shock protein 70.				
GN	HSP70.				
OS	Canis familiaris (dog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
NC	NCBI_TaxID=9615;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Abe K., Kano R., Hasegawa A.;				
RT	"Canine heat shock protein 70 (hsp70) mRNA, complete cds.";				
RL	Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; AB075027; BAB78505.1; -				
DR	InterPro: IPR001023; HSP70.				
DR	Pfam: PF00012; HSP70: 1				
DR	PRINTS: PR00301; HEATSHOCK70.				
DR	PRODOM: PD00089; HSP70: 1.				
DR	PROSITE: PS00297; HSP70_1; UNKNOWN_1.				
DR	PROSITE: PS00329; HSP70_2; UNKNOWN_1.				
DR	PROSITE: PS01036; HSP70_3; UNKNOWN_1.				
DR	SEQUENCE 640 AA: 69935 MW: 402F3E91871BF87F CRC64:				
Query Match	49.6%;	Score 318;	DB 6;	Length 640;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 318;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	96	NDGDKPKVQVSYKGTETKAPPEETSSMTLTKMKETAFAYLGVPTNNAVITPAVFNDSOR	155		
DB	96	NDGDKPKVQVSYKGTETKAPPEETSSMTLTKMKETAFAYLGVPTNNAVITPAVFNDSOR	155		
QY	156	QATKAGVYAGINLVRIINEPTAAIAVGLDRTGKGRNVLLFDLGGGTFFVSIITIDG	215		
DB	156	QATKAGVYAGINLVRIINEPTAAIAVGLDRTGKGRNVLLFDLGGGTFFVSIITIDG	215		

```

QY 216 IFEVKATAGDTLHGGEFDNRLVNHFEVEEKRRKKDISONKRAVRRLPTACERAKRTLS 275
DB 216 IFEVKATAGDTLHGGEFDNRLVNHFEVEEKRRKKDISONKRAVRRLPTACERAKRTLS 275
QY 276 SSTQASLEIDSLFEGIDFTYSTRARPEELCSLFNSTLEPEVKALRDALKDAQIHDLV 335
DB 276 SSTQASLEIDSLFEGIDFTYSTRARPEELCSLFNSTLEPEVKALRDALKDAQIHDLV 335
QY 336 LVGSGRIPIPVOKLLODFEGRDLNKSINDEAVGAQAALMGDKSENVODLLLD 395
DB 336 LVGSGRIPIPVOKLLODFEGRDLNKSINDEAVGAQAALMGDKSENVODLLLD 395
QY 396 VAPLSIGLETAGCVMTAL 413
DB 396 VAPLSIGLETAGCVMTAL 413

RESULT 2
Q90QC1
ID 090QC1 PRELIMINARY; PRT; 151 AA.
AC 090QC1
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Heat shock protein 72 (Fragment).
GN HSP70-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99194576; PubMed-10092532;
RA Shimizu S., Nemura K., Ujihara M., Demura H.;
RT "An additional exon of stress-inducible heat shock protein 70 gene
RT (HSP70-1).";
RL Biochem. Biophys. Res. Commun. 257:193-198(1999).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: AB018045; BAA77235.1; -.
DR HSSP: P03012; 2RSU.
DR InterPro: IPR001023; Hsp70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; Hsp70; 1.
DR PROSITE: PS00329; HSP70_2; 1.
KW ATP-binding.
KW NON_TER
SQ
SEQUENCE 151 AA; 16473 MW; 5C504568DF2CC850 CRC64;

Query Match 23.4%; Score 150; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 2e-146;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 MKHMPFOVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKIEAAYLGYPTNAVITY 146
DB 1 MKHMPFOVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKIEAAYLGYPTNAVITY 60
QY 147 PAFNDSQORATKADAGYIAGLNLRIINEPTAAIAVAGLDRGKGRNVLIPLDGGSTPD 206
DB 61 PAFNDSQORATKADAGYIAGLNLRIINEPTAAIAVAGLDRGKGRNVLIPLDGGSTPD 120
QY 207 VSLFTIDDDGEFEVKATAGDTLHGGEFDNR 236
DB 121 VSLFTIDDDGEFEVKATAGDTLHGGEFDNR 150

RESULT 3
Q63256
ID 063256 PRELIMINARY; PRT; 641 AA.
AC 063256;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
SQ
SEQUENCE 641 AA; 70079 MW; F49C33B602EAE334 CRC64;

```

```

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Heat shock protein 70.
GN HSP 70.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=SPLEEN;
RX MEDLINE-94190258; PubMed-8141767;
RA Westil R., Chi S.H., Sayen W.R., Dillmann W.H.;
RT "Isolation of a novel inducible rat heat shock protein (HSP70) gene
RT and its expression during ischaemia/hypoxia and heat shock.";
RL Biochem. J. 298:561-569(1994).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: X75357; CAA53140.1; -.
DR HSSP: P08107; 1HUO.
DR InterPro: IPR001023; Hsp70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; Hsp70; 1.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding.
KW
SQ
SEQUENCE 641 AA; 69978 MW; A3A1223439AB2D03 CRC64;

Query Match 17.8%; Score 114; DB 11; Length 641;
Best Local Similarity 100.0%; Pred. No. 1.4e-108;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 TLEPVEKALRDALKDAQIHDVLVGSSTRIPIPVOKLLODFEGRDLNKSINDEAVAG 372
DB 313 TLEPVEKALRDALKDAQIHDVLVGSSTRIPIPVOKLLODFEGRDLNKSINDEAVAG 372
QY 373 AAVQAAILMGDKSENVODLLLDVAPLSIGLETAGCVMTALIRNSTIPPKQTQ 426
DB 373 AAVQAAILMGDKSENVODLLLDVAPLSIGLETAGCVMTALIRNSTIPPKQTQ 426

RESULT 4
Q90WU5
ID 090WU5 PRELIMINARY; PRT; 641 AA.
AC 090WU5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE HSP70.
GN H2-BF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R.,
RA Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.;
RT "Sequence of the mouse MHC class III region.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: AF109906; AAC84169.1; -.
DR HSSP: P08107; 1HUO.
DR MGD: MGI:105975; H2-BF.
DR InterPro: IPR001023; Hsp70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; Hsp70; 1.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding.
KW
SQ
SEQUENCE 641 AA; 70079 MW; F49C33B602EAE334 CRC64;

```



QY 448 AMTKDNLLGRF 459  
 DB 450 AMTKDNLLGRF 461

## RESULT 8

Q960C9 PRELIMINARY: PRT: 641 AA.

AC Q960C9; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 GN Heat shock protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.

RA Hirakawa M., Yamaguchi H., Imai K., Shimada J.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.

RA Shihna S., Tamlya G., Oka A., Inoko H.;  
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL: AP000503; BAB63301.1; -

DR InterPro: IPR001023; Hsp70.

DR Pfam: PF000012; Hsp70; 1.

DR PROSITE: PS00297; HSP70\_1; UNKNOWN.1.

DR PROSITE: PS00329; HSP70\_2; UNKNOWN.1.

DR PROSITE: PS01036; HSP70\_3; UNKNOWN.1.

KW ATP-binding.

KM ARF-binding.

SQ SEQUENCE 641 AA; 70405 MW; 303385E7D4300440 CRC64;

Query Match 11.2%; Score 72; DB 4; Length 641;

Best Local Similarity 100.0%; Pred. No. 3.9e-65; Mismatches 0; Indels 0; Gaps 0;

QY 388 VODLLLDVAPISLGETAGVGTALIKRNSIPTRKOTIFTTYSNQPGLVLYVEGER 447  
 DB 390 VODLLLDVAPISLGETAGVGTALIKRNSIPTRKOTIFTTYSNQPGLVLYVEGER 449

QY 448 AMTKDNLLGRF 459  
 DB 450 AMTKDNLLGRF 461

## RESULT 9

Q61698 PRELIMINARY: PRT: 228 AA.

AC Q61698; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

GN Heat shock protein (Hsp68) (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.

RA Lowe D.G., Moran L.A.;  
 RT "Molecular cloning and analysis of DNA complementary to three mouse  
 DR HSP; P08109; ICKR.

DR MGD; MG1:99517; Hsp70-1.  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF000012; Hsp70; 1.  
 DR PRODOM: PD000089; Hsp70; 1.

FT NON\_TER 1 247  
 SQ SEQUENCE 228 AA; 24872 MW; BD7A0931ACE0FEDC CRC64;

Query Match 9.4%; Score 60; DB 11; Length 228;

Best Local Similarity 100.0%; Pred. No. 3.9e-53; Mismatches 0; Indels 0; Gaps 0;

QY 464 IPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITITNDKGLSKEEFIRMTQAE 523  
 DB 50 IPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITITNDKGLSKEEFIRMTQAE 109

## RESULT 10

Q98896 PRELIMINARY: PRT: 247 AA.

AC Q98896; 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

GN Hsp70-1.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Takifugu.

OX NCBI\_TaxID=31033;

RN [1]  
 RP SEQUENCE FROM N.A.

RA MEDLINE=99284127; PubMed=10357235;

RT "Short-range linkage relationships, genomic organization and sequence  
 comparisons of a cluster of five Hsp70 genes in Fugu rubripes."

RL Cell Mol. Life Sci. 55:668-678(1999).

CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

DR EMBL: Y08576; CA69890.1; -

DR HSP; P08107; 1H0.

DR InterPro: IPR001023; Hsp70.

DR Pfam: PF000012; Hsp70; 1.

DR PRINTS: PR00301; HEATSHOCK70.

DR PRODOM: PD000089; Hsp70; 1.

DR PROSITE: PS00297; HSP70\_1; 1.

DR PROSITE: PS00329; HSP70\_2; 1.

KW ATP-binding.

FT NON\_TER 247 247

SQ SEQUENCE 247 AA; 26747 MW; 1F51A895BC941732 CRC64;

Query Match 9.0%; Score 58; DB 13; Length 247;

Best Local Similarity 100.0%; Pred. No. 4.9e-51; Mismatches 0; Indels 0; Gaps 0;

QY 6 AICIDIGTTCYGVGFQHGKVEIIANDGCRTPPSVAFDTFRCLGDAKNOVALNP 63  
 DB 8 AICIDIGTTCYGVGFQHGKVEIIANDGCRTPPSVAFDTFRCLGDAKNOVALNP 65

## RESULT 11

Q73922 PRELIMINARY: PRT: 639 AA.

AC Q73922; 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

GN Hsp70.

OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;

```
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20291066; PubMed=10828441;
RA Molina A., Blemar F., Iyengar A., Prunet P., Maclean N.,
RA Martial J.A., Muller M.;
RT "Cloning and expression analysis of an inducible HSP70 gene from
RT tilapia fish.";
RU FEBS Lett. 474:5-10(2000).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: AJ001312; CA04673.1; -
DR HSSP: P08109; 1CKR.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; HSP70; 1.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding
SQ SEQUENCE 639 AA; 70292 MW; B296FA98407BD4AE CRC64;

Query Match          9.0%; Score 58; DB 13; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AIGDGLTYSVCVGFQHGKVEIIANDGNGRTTSPYAFDTERLIGDAKNOVALNP 63
DB 7 AIGDGLTYSVCVGFQHGKVEIIANDGNGRTTSPYAFDTERLIGDAKNOVALNP 64

RESULT 12
ID Q8UWM9 PRELIMINARY; PRT; 639 AA.
AC Q8UWM9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Stress protein HSP70-2.
GN HSP70-2.
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
CX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamashita M.;
RT "Characterization of multiple members of the HSP70 family in platyfish
RT cultured cells.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB062114; BAB72168.1; -
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; HSP70; 1.
DR PROSITE: PS00297; HSP70_1; UNKNOWN.1.
DR PROSITE: PS00329; HSP70_2; UNKNOWN.1.
SQ SEQUENCE 639 AA; 70128 MW; 87382F59DE5532C CRC64;

Query Match          9.0%; Score 58; DB 13; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
ID Q8UWM8 PRELIMINARY; PRT; 637 AA.
AC Q8UWM8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Stress protein HSC70.
GN HSC70.
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
CX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamashita M.;
RT "Characterization of multiple members of the HSP70 family in platyfish
RT cultured cells.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB062115; BAB72169.1; -
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; HSP70; 1.
DR PROSITE: PS00297; HSP70_1; UNKNOWN.1.
DR PROSITE: PS00329; HSP70_2; UNKNOWN.1.
DR PROSITE: PS01036; HSP70_3; UNKNOWN.1.
SQ SEQUENCE 637 AA; 70567 MW; 6B7BD0245141D3A7 CRC64;

Query Match          8.7%; Score 56; DB 13; Length 637;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GIDGLTYSVCVGFQHGKVEIIANDGNGRTTSPYAFDTERLIGDAKNOVALNP 63
DB 8 GIDGLTYSVCVGFQHGKVEIIANDGNGRTTSPYAFDTERLIGDAKNOVALNP 63

RESULT 14
ID Q9R2A1 PRELIMINARY; PRT; 111 AA.
AC Q9R2A1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Spermatid-specific heat shock protein 70 (fragment).
GN HSP70-3 OR HSC70T.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=129SV/J;
RX MEDLINE=98351992; PubMed=9685725;
RA Ito Y., Ando A., Ando H., Ando J., Saijoh Y., Inoko H., Fujimoto H.;
RT "Genomic structure of the spermatid-specific HSP70 homolog gene
RT located in the class III region of the major histocompatibility
RT complex of mouse and man.";
RL J. Biochem. 124:347-353(1998).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: D85733; BAA32524.1; -
DR MGD: MGI:96244; HSP70-3.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; HSP70; 1.
DR PROSITE: PS00297; HSP70_1; 1.
KW ATP-binding; Heat shock.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12137 MW; A1E912BF92630187 CRC64;

Query Match          8.6%; Score 55; DB 11; Length 111;
```

Best Local Similarity 100.0%; Pred. No. 3e-48; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AIGIDIGTYYSCVGFQHGKVEIANDGCRRTTPTSYAFTDTERLIGDAKNOVA 60  
 |||  
 Db 8 AIGIDIGTYYSCVGFQHGKVEIANDGCRRTTPTSYAFTDTERLIGDAKNOVA 62

RESULT 15

099KD7 PRELIMINARY; PRT; 633 AA.

AC 099KD7; 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)  
 DE Heat shock protein, 70 kDa 2.  
 GN HSP70-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL; BC004714; AA04714.1; .  
 DR HSP; P19120; 3HSC.  
 DR MGD; MGI:96243; Hsp70-2.  
 DR InterPro; IPR001023; Hsp70.  
 DR Pfam; PF00012; Hsp70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR ProDom; PD000089; Hsp70; 1.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW ATP-binding.  
 SQ SEQUENCE 633 AA; 69641 MW; 6F65773C7EFA69F CRC64;

Query Match 8.6%; Score 55; DB 11; Length 633;

Best Local Similarity 100.0%; Pred. No. 1.5e-47; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AIGIDIGTYYSCVGFQHGKVEIANDGCRRTTPTSYAFTDTERLIGDAKNOVA 60  
 |||  
 Db 7 AIGIDIGTYYSCVGFQHGKVEIANDGCRRTTPTSYAFTDTERLIGDAKNOVA 61

Search completed: December 4, 2002, 16:52:44  
 Job time : 40 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:50:58 : Search time 16 Seconds  
(without alignments)  
1178.736 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 641  
Sequence: 1 MAKAAIGIDIGTTCVGV.....FGAGPKGSGSGPTIEVD 641

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/laa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/laa/5A.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/laa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/laa/6A.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/laa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/laa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	8.3	646	1	US-08-441-139-14
2	53	8.3	890	4	US-09-513-783A-174
3	47	7.3	643	4	US-08-797-358B-3
4	28	4.4	339	2	US-08-928-692-52
5	28	4.4	339	4	US-08-339-972-52
6	23	3.6	679	1	US-08-214-583-2
7	20	3.1	315	1	US-08-257-073-7
8	19	3.0	649	4	US-09-066-047-5
9	18	2.8	18	1	US-08-240-514-37
10	18	2.8	18	2	US-08-612-302A-37
11	18	2.8	616	4	US-08-134-001C-3646
12	18	2.8	635	4	US-09-632-538C-36
13	17	2.7	17	2	US-08-480-190-132
14	17	2.7	17	2	US-08-488-379-132
15	17	2.7	17	5	PCT-US93-07545-132
16	16	2.5	42	6	5196523-15
17	16	2.5	80	1	US-08-464-164-4
18	16	2.5	80	1	US-08-338-057-4
19	16	2.5	80	2	US-08-668-416-4
20	16	2.5	187	6	5196523-13
21	16	2.5	654	1	US-08-441-139-11
22	16	2.5	663	1	US-08-441-139-7
23	16	2.5	666	1	US-08-441-139-16
24	16	2.5	682	1	US-08-441-139-2
25	15	2.3	15	2	US-08-480-190-133
26	15	2.3	15	2	US-08-488-379-133
27	15	2.3	15	5	PCT-US93-07545-133

28	15	2.3	79	6	5196523-11	Patent No. 5196523
29	15	2.3	168	4	US-08-441-139-10	Sequence 10, Appl
30	15	2.3	183	4	US-09-556-877-301	Sequence 301, App
31	15	2.3	183	4	US-09-620-412C-301	Sequence 301, App
32	15	2.3	641	1	US-08-441-139-4	Sequence 4, Appl1
33	15	2.3	679	1	US-08-441-139-5	Sequence 5, Appl1
34	13	2.0	13	6	5196523-19	Patent No. 5196523
35	13	2.0	607	2	US-08-472-534-5	Sequence 5, Appl1
36	12	1.9	77	6	5196523-7	Patent No. 5196523
37	11	1.7	11	6	5196523-14	Patent No. 5196523
38	11	1.7	11	6	5196523-18	Patent No. 5196523
39	11	1.7	18	6	5196523-17	Patent No. 5196523
40	11	1.7	129	6	5196523-10	Patent No. 5196523
41	10	1.6	10	6	5196523-16	Patent No. 5196523
42	10	1.6	11	6	5464750-1	Patent No. 5464750
43	10	1.6	41	6	5196523-6	Patent No. 5196523
44	10	1.6	307	4	US-08-858-207A-481	Sequence 481, App
45	10	1.6	471	1	US-08-203-905B-2	Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-441-139-14  
Sequence 14, Application US/08441139  
Patent No. 5773245  
GENERAL INFORMATION:  
APPLICANT: Wiltup, Dr. Karl D.  
APPLICANT: Robinson, Anne S.  
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF  
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: USA  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,139  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/089,997  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 646 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-441-139-14  
Query Match 8.3%; Score 53; DB 1; Length 646;  
Best Local Similarity 100.0%; Pred. No. 3e-45;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 GIDGTTSCVGVFQHGKVEIIANDQGNRTTPSYAFIDTERLIGDAKNOVA 60

```
DB      8 GIDLGTTSCVGFQHGKVEIIANDGNNRTPTSYAFTDTERLIGDAKNOVA 60
      |||||||
RESULT 2
US-09-513-783A-174
; Sequence 174, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-11
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 174
; LENGTH: 890
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70
US-09-513-783A-174
Query Match      8.3%; Score 53; DB 4; Length 890;
Best Local Similarity 100.0%; Pred. No. 4.2e-45;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

-QY      8 GIDLGTTSCVGFQHGKVEIIANDGNNRTPTSYAFTDTERLIGDAKNOVA 60
      |||||||
DB      252 GIDLGTTSCVGFQHGKVEIIANDGNNRTPTSYAFTDTERLIGDAKNOVA 304

RESULT 3
US-08-797-358B-3
; Sequence 3, Application US/08797358B
; Patent No. 6268478
; GENERAL INFORMATION:
; APPLICANT: Adams, John
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,358B
; FILING DATE: 11-Feb-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,491
; FILING DATE: 12-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CE 3165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 643 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
```

```
      ; TOPOLOGY: unknown
      ; MOLECULE TYPE: protein
      ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
Query Match      7.3%; Score 47; DB 4; Length 643;
Best Local Similarity 100.0%; Pred. No. 3.9e-39;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

-QY      440 IOYBESRAMTKDNNLGRFELSGTPAPRGVQITFVEDIDANGIL 486
      |||||||
DB      442 IOYBESRAMTKDNNLGRFELSGTPAPRGVQITFVEDIDANGIL 488

RESULT 4
US-08-928-692-52
; Sequence 52, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Iamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Iambirlis, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
US-08-928-692-52
Query Match      4.4%; Score 28; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 4.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

-QY      214 DGIPEYKATAGDTHUGGEDFDNRLVNH 241
      |||||||
DB      211 DGIPEYKATAGDTHUGGEDFDNRLVNH 238

RESULT 5
US-09-339-972-52
; Sequence 52, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
```

APPLICANT: Yaver, Deborah S.  
APPLICANT: Lamsa, Michael  
APPLICANT: Hansen, Kim  
TITLE OF INVENTION: Methods for Modifying the Production of  
TITLE OF INVENTION: a Polypeptide  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/339,972  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/928,692  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lambiris, Elias J  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 4944.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 6323002e  
US-09-339-972-52

Query Match 4.4%; Score 28; DB 4; Length 339;  
Best Local Similarity 100.0%; Pred. No. 4.6e-20;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 DGIPEVKATAGDTHLGGEEDPNRLVNH 241  
DB 211 DGIPEVKATAGDTHLGGEEDPNRLVNH 238

RESULT 6  
US-08-214-583-2  
Sequence 2, Application US/08214583  
Patent No. 5627039  
GENERAL INFORMATION:  
APPLICANT: Pereira-Smith, Olivia  
APPLICANT: Madhwa, Renu  
TITLE OF INVENTION: MORFALIN AND METHODS FOR DETERMINING  
TITLE OF INVENTION: COMPLEMENTATION GROUP ASSIGNMENT OF CANCER CELLS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Howrey & Simon  
STREET: 1299 Pennsylvania Ave, NW  
CITY: Washington  
STATE: DC  
COUNTRY: US  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/214,583  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Auerbach, Jeffrey I.  
REGISTRATION NUMBER: 32,680  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-383-7451  
TELEFAX: 202-383-6610  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 679 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Murine  
IMMEDIATE SOURCE:  
CLONE: mortalain  
US-08-214-583-2

Query Match 3.6%; Score 23; DB 1; Length 679;  
Best Local Similarity 100.0%; Pred. No. 1.1e-14;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 GIPPADRGVQIEVTPDIDANGI 485  
DB 507 GIPPADRGVQIEVTPDIDANGI 529

RESULT 7  
US-08-257-073-7  
Sequence 7, Application US/08257073  
Patent No. 5766597  
GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
APPLICANT: de Taisne, Charles  
APPLICANT: Tine, John A.  
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE  
NUMBER OF SEQUENCES: 143  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue, 25th Floor  
CITY: New York  
STATE: New York  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/257,073  
FILING DATE: 09-JUN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/075,783  
FILING DATE: 11-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/852,305  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/672,183  
FILING DATE: 20-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2570  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712  
TELEX: 425066 CURTMS  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 315 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-257-073-7

Query Match 3.1%; Score 20; DB 1; Length 315;  
Best Local Similarity 100.0%; Pred. No. 6e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 VPOIEVTFDIDANGILNVTA 490  
DB 118 VPOIEVTFDIDANGILNVTA 137

## RESULT 8

US-09-066-047-5  
Sequence 5, Application US/09066047A  
Patent No. 6306394  
GENERAL INFORMATION:  
APPLICANT: MURPHY, Cheryl  
BELTZ, Gerald A.  
COUGHLIN, Richard T.  
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF  
USE OF GRANULOCYTIC EHRLLICHA  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: United States  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/066,047A  
FILING DATE: 24-Apr-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/044,869  
FILING DATE: 25-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Superko, Colleen  
REGISTRATION NUMBER: 39,850  
REFERENCE/DOCKET NUMBER: 106,941.156  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 649 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-066-047-5

Query Match 3.0%; Score 19; DB 4; Length 649;  
Best Local Similarity 100.0%; Pred. No. 1.3e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 APRGVPQIEVTFDIDANGI 485  
DB 463 APRGVPQIEVTFDIDANGI 481

## RESULT 9

US-08-240-514-37  
Sequence 37, Application US/08240514  
Patent No. 5670347  
GENERAL INFORMATION:  
APPLICANT: GOPAL, T. Venkat  
TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/240,514  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 73521/102/CLIN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-240-514-37

Query Match 2.8%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 FKRRKKRDISONKRAVRR 262  
DB 1 FKRRKKRDISONKRAVRR 18

## RESULT 10

US-08-612-302A-37  
Sequence 37, Application US/08612302A  
Patent No. 5811297  
Patent No. 5811297 5780297  
GENERAL INFORMATION:  
APPLICANT: GOPAL, T. Venkat  
TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
STREET: One Westlakes, Berwyn  
CITY: Valley Forge  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,302A  
FILING DATE: 7 March 1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: AMBA-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 407-0700  
TELEFAX: (610) 407-0701  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: n.a.  
US-08-612-302A-37

Query Match 2.8%; Score 18; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 245 FKRKKKDISONKRAVR 262  
Db 1 FKRKKKDISONKRAVR 18

RESULT 11  
US-09-134-001C-3646  
Sequence 3646, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3646  
LENGTH: 616  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3646

Query Match 2.8%; Score 18; DB 4; Length 616;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 464 IPPAPRGVQIEVTFDID 481  
Db 439 IPPAPRGVQIEVTFDID 456

RESULT 12  
US-09-632-538C-36  
Sequence 36, Application US/09632538C  
Patent No. 6440674  
GENERAL INFORMATION:  
APPLICANT: Mista, Santosh et al  
TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH  
FILE REFERENCE: 54359  
CURRENT APPLICATION NUMBER: US/09/632,538C  
CURRENT FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 37  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 36  
LENGTH: 655  
TYPE: PRT  
ORGANISM: Pseudotsuga menziesii  
US-09-632-538C-36

Query Match 2.8%; Score 18; DB 4; Length 655;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 461 LSGIPAPRGVQIEVTF 478  
Db 483 LSGIPAPRGVQIEVTF 500

RESULT 13  
US-08-480-190-132  
Sequence 132, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Darlo A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555x  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-132

Query Match 2.7%; Score 17; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 38 TPSYVAFDTERTLIGDA 54  
|||||

Db 1 TSPSYVAFTDTERLIGDA 17

RESULT 14

US-08-488-379-132

Sequence 132, Application US/08488379

Patent No. 5880103

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Dario A. A. Vignali

APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,379

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,255

FILING DATE: June 15, 1993

APPLICATION NUMBER: 07/925,460

FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ. ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 17

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-488-379-132

Query Match 2.7%; Score 17; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e-10;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TSPSYVAFTDTERLIGDA 54

Db 1 TSPSYVAFTDTERLIGDA 17

RESULT 15

PCT-US93-07545-132

Sequence 132, Application PC/TUS9307545

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Dario A. A. Vignali

APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern

APPLICANT: Jack L. Strominger

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07545

FILING DATE: 19930811

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/925,460

FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ. ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 17

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US93-07545-132

Query Match 2.7%; Score 17; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e-10;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TSPSYVAFTDTERLIGDA 54

Db 1 TSPSYVAFTDTERLIGDA 17

Search completed: December 4, 2002, 16:53:35

Job time : 18 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:35:46 : Search time 14 Seconds

(without alignments) updates/sec  
1899.023 Million cell

Title: US-09-646-835-1

Perfect score: 3263  
Sequence: 1 MAKAAIGIDGTTYSYCVG.....FGAAGPKGSGSGPTIEVD 641

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3263	100.0	641	HS71_HUMAN	P08107 homo sapien
2	3225	98.8	641	HS72_BOVIN	Q27965 bos taurus
3	3216	98.5	641	HS71_BOVIN	Q27975 bos taurus
4	3182	97.5	641	HS71_PIG	P34930 sus scrofa
5	3160	96.8	641	HS71_RAT	Q07439 ratus norv
6	3148.5	96.5	638	HS71_CERAE	Q28222 cercopithec
7	3130	95.9	641	HS71_MOUSE	P17879 mus musculu
8	2921	89.5	641	HS71_HUMAN	P34931 homo sapien
9	2887	88.5	641	HS71_MOUSE	P16627 mus musculu
10	2882	88.3	641	HS73_RAT	P55063 ratus norv
11	2862.5	87.7	646	HS7C_MOUSE	P08109 mus musculu
12	2859.5	87.6	646	HS7C_HUMAN	P11142 homo sapien
13	2853.5	87.5	650	HS7C_BOVIN	P19120 bos taurus
14	2843.5	87.1	646	HS7C_CRIGR	P02970 cricetus
15	2835.5	86.9	647	HS70_XENLA	P02827 xenopus lae
16	2816	86.3	651	HS70_ONCMY	P08108 oncohychnu
17	2812	86.2	649	HS7C_BRARE	Q09473 brachydantio
18	2810.5	86.1	644	HS70_ONCTS	Q09123 oncohychnu
19	2798	85.7	643	HS76_PIG	Q04967 sus scrofa
20	2789.5	85.5	652	HS7D_MANSE	Q09139 manduca sex
21	2785	85.4	639	HS71_ORYLA	Q09189 oryza lat
22	2776	85.1	649	HS7C_ICTPU	P47773 ictalurus p
23	2772.5	85.0	639	HS72_HUMAN	P54652 homo sapien
24	2766	84.8	634	HS70_PLEWA	Q01291 pleurodeles
25	2755.5	84.6	633	HS70_CHICK	P08106 gallus gall
26	2754.5	84.4	633	HS72_RAT	P17156 ratus norv
27	2747	84.2	643	HS72_MOUSE	P17066 homo sapien
28	2737	83.9	651	HS7D_HUMAN	P11147 drosophila
29	2735	83.8	644	HS70_BRUMA	P27541 brugia mala
30	2697.5	82.7	631	HS73_BOVIN	P34933 bos taurus
31	2678.5	82.1	686	HS7C_ORYLA	Q09471 oryza lat
32	2670.5	81.8	654	HS70_HYDMA	Q05444 hydra magni

34	2664	81.6	641	HS7A_DROME	P29843 drosophila
35	2658.5	81.5	640	HS7A_CAEEL	P09446 caenorhabdi
36	2614	80.1	637	HS70_SCHNA	P08418 schistosoma
37	2565.5	78.6	640	HS74_ANOAL	P41827 anopheles a
38	2544.5	78.0	640	HS71_PUCGR	Q01877 puccinia gr
39	2541.5	77.9	640	HS71_ANOAL	P41825 anopheles a
40	2538.5	77.8	640	HS72_ANOAL	P41826 anopheles a
41	2519.5	77.2	651	HS7C_PETRY	P09189 petunia hyb
42	2514.5	77.1	643	HS71_SCHFO	Q10265 schizosach
43	2513.5	77.0	651	HS71_ARATH	P22953 arabidopsis
44	2504	76.7	642	HS70_DROME	P82910 drosophila
45	2502.5	76.7	641	HS72_DROME	P08284 drosophila

## ALIGNMENTS

RESULT 1  
ID HS71\_HUMAN STANDARD: PRT: 641 AA.  
AC P08107; P19790; Q9U0M0; Q9U0L9;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).  
GN (HSPA1A OR HSPA1) AND HSPA1B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE-91055806; PubMed-1700760;  
RA Milner C.M., Campbell R.D.;  
RT "Structure and expression of the three MHC-linked HSP70 genes.";  
RL Immunogenetics 32:242-251(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-86016721; PubMed-3931075;  
RA Hunt C., Morimoto R.I.;  
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).  
RN [3]  
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).  
RA Rowen L., Madan A., Qin S., Shafer T., James R., Ratcliffe A.,  
RA Abbasi N., Dichtoff R., Loretz C., Madan A., Dors M., Young J.,  
RA Laskey S., Hood L.;  
RT "Sequence of the human major histocompatibility complex class III region.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).  
RX Shihna S., Tamuya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.  
RX MEDLINE-89184548; PubMed-2538825;  
RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;  
RT "Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).  
RN [6]  
RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.  
RX MEDLINE-87066768; PubMed-3786141;  
RA Drebert B., Genthe A., Bencke B.-J.;  
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";  
RL Nucleic Acids Res. 14:8933-8949(1986).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.  
RX MEDLINE-99234376; PubMed-10216320;

RA Osiptuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;  
 RT Structure of a new crystal form of human hsp70 ATPase domain.";  
 RL Acta Crystallogr. D 55:1105-1107(1999).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
 CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
 CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
 CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
 CC CONFORMATION OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
 CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
 CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
 CC STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M59828; AAA63226.1; -;  
 DR EMBL: M59830; AAA63227.1; -;  
 DR EMBL: AP134726; AAD21816.1; -;  
 DR EMBL: AP134726; AAD21815.1; -;  
 DR EMBL: AP000503; BAB63300.1; -;  
 DR EMBL: AP000503; BAB63299.1; -;  
 DR EMBL: M11717; AAA52697.1; -;  
 DR EMBL: M24743; AAA59844.1; -;  
 DR EMBL: M24744; AAA59845.1; -;  
 DR EMBL: X04676; CAA28381.1; -;  
 DR EMBL: X04677; CAA28382.1; -;  
 DR PIR: A29160; A29160.  
 DR PIR: A45871; A45871.  
 DR PIR: A25773; A25773.  
 DR PDB: 1H0D; 21-OCT-98.  
 DR SWISS-2DPAGE; P08107; HUMAN.  
 DR Genew; HGNC:5232; HSPA1A.  
 DR Genew; HGNC:5233; HSPA1B.  
 DR MIM; 140550; -;  
 DR MIM; 603012; -;  
 DR InterPro; IPR001023; Hsp70.  
 DR Pfam; PF000012; HSP70.1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR ProDom; PD000089; Hsp70.1.  
 DR PROSITE; PS00297; HSP70.1; 1.  
 DR PROSITE; PS00329; HSP70.2; 1.  
 DR PROSITE; PS01036; HSP70.3; 1.  
 KW ATP-binding; Chaperone; Heat shock; Multigene family;  
 KW 3D-structure.  
 FT CONFLICT 7 7 I -> V (IN REF. 2).  
 FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).  
 FT CONFLICT 370 370 A -> G (IN REF. 2).  
 FT CONFLICT 469 469 MISSING (IN REF. 2).  
 FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).  
 SQ SEQUENCE 641 AA: 78FS13118C96D66 CRC64;  
 Query Match 100.0%; Score 3263; DB 1; Length 641;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-174;  
 Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 SMVLTKKKEIAEAVLYGYPYNAVITVPAYENDSORQATKAGYIAGLNVLRINEPTAA 180  
 DB 121 SMVLTKKKEIAEAVLYGYPYNAVITVPAYENDSORQATKAGYIAGLNVLRINEPTAA 180  
 QY 181 IAYGLDRTGGERNVLIEDIIGGTFDVSILITDGEFEVKAIVAGDTHLGEDFDNRLVNH 240  
 DB 181 IAYGLDRTGGERNVLIEDIIGGTFDVSILITDGEFEVKAIVAGDTHLGEDFDNRLVNH 240  
 QY 241 FVEEFKRRKKDSONRAVRRLTACERAKRTLSSSTQSLFEDSLFEGIDETYSTRA 300  
 DB 241 FVEEFKRRKKDSONRAVRRLTACERAKRTLSSSTQSLFEDSLFEGIDETYSTRA 300  
 QY 301 RFEEELCSDFRSTLEPEYERAKLRPAKLDKAOIHLVLVGSGSTRIPKVKLLQDFENGNDLN 360  
 DB 301 RFEEELCSDFRSTLEPEYERAKLRPAKLDKAOIHLVLVGSGSTRIPKVKLLQDFENGNDLN 360  
 QY 361 KSINPDEAVAYGAAYCAATIMGKSENVODLLIDVAPLSLGETAGVNTALIKRSTI 420  
 DB 361 KSINPDEAVAYGAAYCAATIMGKSENVODLLIDVAPLSLGETAGVNTALIKRSTI 420  
 QY 421 PTKOTQFTTYSNDQPEVLIQVTEGERAMTKDNNLGRFELSGIPPAKGVPOIEVTFDI 480  
 DB 421 PTKOTQFTTYSNDQPEVLIQVTEGERAMTKDNNLGRFELSGIPPAKGVPOIEVTFDI 480  
 QY 481 DANGILNVATDKSTGKANKITTTNDKGRLSKEIERMVOAEKRYKADEVOREYSANK 540  
 DB 481 DANGILNVATDKSTGKANKITTTNDKGRLSKEIERMVOAEKRYKADEVOREYSANK 540  
 QY 541 ALESYAFNMKSAYEDBGLKRISEADKKKVLKCOEYISWLDANTLAKEFEHKKRELE 600  
 DB 541 ALESYAFNMKSAYEDBGLKRISEADKKKVLKCOEYISWLDANTLAKEFEHKKRELE 600  
 QY 601 QVCNPITISGLYOGAGPGPGFAGQPGKGGSGSGPTIEVD 641  
 DB 601 QVCNPITISGLYOGAGPGPGFAGQPGKGGSGSGPTIEVD 641  
 RESULT 2  
 HS72\_BOVIN STANDARD; PRT: 641 AA.  
 ID HS72\_BOVIN STANDARD; PRT: 641 AA.  
 AC Q27965; Q28122;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Heat shock 70 kDa protein 2 (Hsp70-2).  
 GN HSP70-2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Angus;  
 RA Grosz M.D., Skow L.C.;  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-28 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94070117; PubMed=8249428;  
 RA Kowalski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,  
 RA van den Hurk J., Bablok L.A., Zamb T.J.;  
 RT "Heat-shock promoter-driven synthesis of secreted bovine herpesvirus  
 RT glycoproteins in transfected cells.";  
 RL Vaccine 11:1100-1107(1993).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
 CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
 CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE



PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
CONFORMATION OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
STRESS-INDUCED DAMAGE.  
-1- INDUCTION: BY HEAT SHOCK.  
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: U02892; AAA03451.1; -;  
CC EMBL: M98823; AAA30568.1; -;  
CC HSSP: P08107; 1H0O.  
CC InterPro: IPR001023; Hsp70.  
CC Pfam: PF00012; HSP70\_1.  
CC PRINTS: PR00301; HEATSHOCK70.  
CC ProDom: PD000089; Hsp70\_1.  
CC PROSITE: PS00297; HSP70\_1; 1.  
CC PROSITE: PS00329; HSP70\_2; 1.  
CC PROSITE: PS01036; HSP70\_3; 1.  
CC ATP-binding; Chaperone; Heat shock; Multigene family.  
CC KW  
CC SEQUENCE 641 AA; 70228 MW; 229C19EBBF610DF CRC64;  
-----  
Query Match 98.8%; Score 3225; DB 1; Length 641;  
Best Local Similarity 98.9%; Pred. No. 1; le-171;  
Matches 634; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
-----  
QY 1 MAKAAAGIDLTGTTSCVGFQHGKVEIIANDQGNFTTPSYAFDTERRLIGDAKNOYA 60  
DB 1 MAKNAIGIDLTGTTSCVGFQHGKVEIIANDQGNFTTPSYAFDTERRLIGDAKNOYA 60  
QY 61 LNPQNTVPARKRLIGKREDDPVVQSDMKMPROVINIDGKPPVQVSYKETAFAFYEEIS 120  
DB 61 LNPQNTVPARKRLIGKREDDPVVQSDMKMPRPVINDGKPPVQVSYKETAFAFYEEIS 120  
QY 121 SMVLTQMKELIAYVLYGYPNTNAVITYPAFVNDQSOQATDAGVAGLVNLRINPTAA 180  
DB 121 SMVLTQMKELIAYVLYGYPNTNAVITYPAFVNDQSOQATDAGVAGLVNLRINPTAA 180  
QY 121 SMVLTQMKELIAYVLYGYPNTNAVITYPAFVNDQSOQATDAGVAGLVNLRINPTAA 180  
DB 121 SMVLTQMKELIAYVLYGYPNTNAVITYPAFVNDQSOQATDAGVAGLVNLRINPTAA 180  
QY 181 IAYGLDRGKGRNVLIFDLGGTGVDSILTTIDGIFEVKATPAGDTHLGGEDFNRLVNH 240  
DB 181 IAYGLDRGKGRNVLIFDLGGTGVDSILTTIDGIFEVKATPAGDTHLGGEDFNRLVNH 240  
QY 181 IAYGLDRGKGRNVLIFDLGGTGVDSILTTIDGIFEVKATPAGDTHLGGEDFNRLVNH 240  
DB 181 IAYGLDRGKGRNVLIFDLGGTGVDSILTTIDGIFEVKATPAGDTHLGGEDFNRLVNH 240  
QY 241 PVEEFRRKKKDISONKRRVRLRTACERAKRTLSSTQASLEISLFGIDFYTSTTA 300  
DB 241 PVEEFRRKKKDISONKRRVRLRTACERAKRTLSSTQASLEISLFGIDFYTSTTA 300  
QY 241 PVEEFRRKKKDISONKRRVRLRTACERAKRTLSSTQASLEISLFGIDFYTSTTA 300  
DB 241 PVEEFRRKKKDISONKRRVRLRTACERAKRTLSSTQASLEISLFGIDFYTSTTA 300  
QY 301 REELCSDFRSTLEFEVERKALDKAQAIDHVLVGGSTPIPKYQKLLQDFPFGNDLN 360  
DB 301 REELCSDFRSTLEFEVERKALDKAQAIDHVLVGGSTPIPKYQKLLQDFPFGNDLN 360  
QY 301 REELCSDFRSTLEFEVERKALDKAQAIDHVLVGGSTPIPKYQKLLQDFPFGNDLN 360  
DB 301 REELCSDFRSTLEFEVERKALDKAQAIDHVLVGGSTPIPKYQKLLQDFPFGNDLN 360  
QY 361 KSIINDEAVAYGAOVAAILMGDKSENVDLLIDVAPLSLGLFAGVWALIKENSTT 420  
DB 361 KSIINDEAVAYGAOVAAILMGDKSENVDLLIDVAPLSLGLFAGVWALIKENSTT 420  
QY 421 PKKQFIPTTSDNOGVLIQVYEGGERAMTKNNNLGRELSGIPAPRGVQIETFPDI 480  
DB 421 PKKQFIPTTSDNOGVLIQVYEGGERAMTKNNNLGRELSGIPAPRGVQIETFPDI 480  
QY 481 DANGILNATATDKSTGKANKIITNDKRLSKEELERMOEAKEKYAEDVEQERYSARN 540  
DB 481 DANGILNATATDKSTGKANKIITNDKRLSKEELERMOEAKEKYAEDVEQERYSARN 540  
QY 541 ALESTAFNNKSAVEDGKLGKISEADKKVLDKCOEVIWLDANTLAEKDEFHKKRELE 600  
DB 541 ALESTAFNNKSAVEDGKLGKISEADKKVLDKCOEVIWLDANTLAEKDEFHKKRELE 600

QY 601 QVCNPIISGLYAGAGPGGFGAGCPKGGSGSGPTIEVD 641  
DB 601 QVCNPIISGLYAGAGPGGFGAGCPKGGSGSGPTIEVD 641  
-----  
RESULT 3  
HS71\_BOVIN STANDARD; PRT; 641 AA.  
ID HS71\_BOVIN  
AC Q27975; Q27964; (rel. 35, Created)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DE Heat shock 70 kDa protein 1 (HSP70-1).  
GN HSP70-1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=95126904; PubMed=7826329;  
RA Gutierrez J.A., Guerrero V.;  
RT "Chemical modifications of a recombinant bovine stress-inducible 70  
kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";  
RL Biochem. J. 305:197-203(1995).  
RN [2]  
RP SEQUENCE OF 212-641 FROM N.A.  
RC STRAIN=Angus;  
RX MEDLINE=95030563; PubMed=7943958;  
RA Grosz M.D., Skow L.C., Stone R.T.;  
RT "An Alu polymorphism at the bovine 70 kD heat-shock protein-1  
(Hsp70-1) locus.";  
RL Anim. Genet. 25:196-196(1994).  
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRYING FORCE FOR  
PROTEIN TRANSLATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
STRESS-INDUCED DAMAGE.  
CC -1- INDUCTION: BY HEAT SHOCK.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: U02891; AAA03450.1; -;  
CC EMBL: U02891; AAA03450.1; -;  
CC HSSP: P08107; 1H0O.  
CC InterPro: IPR001023; Hsp70.  
CC Pfam: PF00012; HSP70\_1.  
CC PRINTS: PR00301; HEATSHOCK70.  
CC ProDom: PD000089; Hsp70\_1.  
CC PROSITE: PS00297; HSP70\_1; 1.  
CC PROSITE: PS00329; HSP70\_2; 1.  
CC PROSITE: PS01036; HSP70\_3; 1.  
CC ATP-binding; Chaperone; Heat shock; Multigene family.  
CC KW  
CC SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;  
-----  
Query Match 98.6%; Score 3216; DB 1; Length 641;  
Best Local Similarity 98.8%; Pred. No. 3; le-171;  
-----

Matches 633; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAKAAAGIDIGTTCVGVQHGKVELIANDOGNRTTPSYAFTDRLIGDAKNQVA 60  
 DB 1 MAKMAAGIDIGTTCVGVQHGKVELIANDOGNRTTPSYAFTDRLIGDAKNQVA 60  
 QY 61 LNPONTVPDAKRLIGRKGDPVVDGKHPFQYINDGKRYOVSYKGETKAFYPERIS 120  
 DB 61 LNPONTVPDAKRLIGRKGDPVVDGKHPFQYINDGKRYOVSYKGETKAFYPERIS 120  
 QY 121 SMVLTKKKEIAEALYGPVTNAVTTPAYFNDGQKATKQAGVAGLVNLIINEPTAA 180  
 DB 121 SMVLTKKKEIAEALYGPVTNAVTTPAYFNDGQKATKQAGVAGLVNLIINEPTAA 180  
 QY 181 IAYGLDRGKERVNLIFDLGGTFDVSILITIDGIEFKVATADTHLGGEDFNRLVNH 240  
 DB 181 IAYGLDRGKERVNLIFDLGGTFDVSILITIDGIEFKVATADTHLGGEDFNRLVNH 240  
 QY 241 FVEEFKRRKKKDIQONKRAVRRLTACBRARLTSSSTQASLEIDSLFEGIDFTSTRA 300  
 DB 241 FVEEFKRRKKKDIQONKRAVRRLTACBRARLTSSSTQASLEIDSLFEGIDFTSTRA 300  
 QY 301 RFEELCSDFRSTLEPEKALRDALDKAQTHDLVVGSGTRIRKVOKLDDPFNGRDLN 360  
 DB 301 RFEELCSDFRSTLEPEKALRDALDKAQTHDLVVGSGTRIRKVOKLDDPFNGRDLN 360  
 QY 361 KSINPDEAVAGAVOAAILMGDSKENVODLLDLVAPLSGLETAGVMTALIKRNTI 420  
 DB 361 KSINPDEAVAGAVOAAILMGDSKENVODLLDLVAPLSGLETAGVMTALIKRNTI 420  
 QY 421 PTKOTOFTTYSNDQPGVLIQYGERAMTKDNLLGFEISGLIPPRAGVPOLEVFEDI 480  
 DB 421 PTKOTOFTTYSNDQPGVLIQYGERAMTKDNLLGFEISGLIPPRAGVPOLEVFEDI 480  
 QY 481 DANGILNVTATDKSTGKANKTTITNDGRLSKKEIERMVOGAERYKKADEVOREVSAGN 540  
 DB 481 DANGILNVTATDKSTGKANKTTITNDGRLSKKEIERMVOGAERYKKADEVOREVSAGN 540  
 QY 541 ALESYAFNMKSAVEDEGLKGISPADKKKVLKCOEYISWLDANTLAEKDEFEHKKRELE 600  
 DB 541 ALESYAFNMKSAVEDEGLKGISPADKKKVLKCOEYISWLDANTLAEKDEFEHKKRELE 600  
 QY 601 QVCNPIISGLYOGAGGPGGFGAGQPKGSGSGPTIEVD 641  
 DB 601 QVCNPIISGLYOGAGGPGGFGAGQPKGSGSGPTIEVD 641

RESULT 4  
 HS71\_PIG STANDARD; PRT; 641 AA.

AC P34930;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Heat shock 70 kDa protein 1 (HSP70.1).  
 GN HSP70.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92175874; PubMed=1339404;  
 RA Peelman L.J., de Waele A.R., Coppieters W.R., van Zeveren A.J.,  
 RA Bouquet Y.H.;  
 RT "Complete nucleotide sequence of a porcine HSP70 gene";  
 RL Immunogenetics 35:286-289(1992).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET

CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M69100; ; NOT ANNOTATED; CDS.  
 DR PIR: S35718; S35718.  
 DR HSP: P08107; 1H0.  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PRODOM: PD000089; Hsp70; 1.  
 DR PROSITE: PS00297; HSP70.1; 1.  
 DR PROSITE: PS00329; HSP70.2; 1.  
 DR PROSITE: PS01036; HSP70.3; 1.  
 KW ATP-binding; Chaperone; Heat shock; Multigene family;  
 KW SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A53 CRC64;

Query Match 97.5%; Score 3182; DB 1; Length 641;  
 Best local similarity 97.3%; Pred. No. 2.6e-169;  
 Matches 624; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAKAAAGIDIGTTCVGVQHGKVELIANDOGNRTTPSYAFTDRLIGDAKNQVA 60  
 DB 1 MAKMAAGIDIGTTCVGVQHGKVELIANDOGNRTTPSYAFTDRLIGDAKNQVA 60  
 QY 61 LNPONTVPDAKRLIGRKGDPVVDGKHPFQYINDGKRYOVSYKGETKAFYPERIS 120  
 DB 61 LNPONTVPDAKRLIGRKGDPVVDGKHPFQYINDGKRYOVSYKGETKAFYPERIS 120  
 QY 121 SMVLTKKKEIAEALYGPVTNAVTTPAYFNDGQKATKQAGVAGLVNLIINEPTAA 180  
 DB 121 SMVLTKKKEIAEALYGPVTNAVTTPAYFNDGQKATKQAGVAGLVNLIINEPTAA 180  
 QY 181 IAYGLDRGKERVNLIFDLGGTFDVSILITIDGIEFKVATADTHLGGEDFNRLVNH 240  
 DB 181 IAYGLDRGKERVNLIFDLGGTFDVSILITIDGIEFKVATADTHLGGEDFNRLVNH 240  
 QY 241 FVEEFKRRKKKDIQONKRAVRRLTACBRARLTSSSTQASLEIDSLFEGIDFTSTRA 300  
 DB 241 FVEEFKRRKKKDIQONKRAVRRLTACBRARLTSSSTQASLEIDSLFEGIDFTSTRA 300  
 QY 301 RFEELCSDFRSTLEPEKALRDALDKAQTHDLVVGSGTRIRKVOKLDDPFNGRDLN 360  
 DB 301 RFEELCSDFRSTLEPEKALRDALDKAQTHDLVVGSGTRIRKVOKLDDPFNGRDLN 360  
 QY 361 KSINPDEAVAGAVOAAILMGDSKENVODLLDLVAPLSGLETAGVMTALIKRNTI 420  
 DB 361 KSINPDEAVAGAVOAAILMGDSKENVODLLDLVAPLSGLETAGVMTALIKRNTI 420  
 QY 421 PTKOTOFTTYSNDQPGVLIQYGERAMTKDNLLGFEISGLIPPRAGVPOLEVFEDI 480  
 DB 421 PTKOTOFTTYSNDQPGVLIQYGERAMTKDNLLGFEISGLIPPRAGVPOLEVFEDI 480  
 QY 481 DANGILNVTATDKSTGKANKTTITNDGRLSKKEIERMVOGAERYKKADEVOREVSAGN 540  
 DB 481 DANGILNVTATDKSTGKANKTTITNDGRLSKKEIERMVOGAERYKKADEVOREVSAGN 540  
 QY 541 ALESYAFNMKSAVEDEGLKGISPADKKKVLKCOEYISWLDANTLAEKDEFEHKKRELE 600  
 DB 541 ALESYAFNMKSAVEDEGLKGISPADKKKVLKCOEYISWLDANTLAEKDEFEHKKRELE 600  
 QY 601 QVCNPIISGLYOGAGGPGGFGAGQPKGSGSGPTIEVD 641  
 DB 601 QVCNPIISGLYOGAGGPGGFGAPDLKGGSGSGPTIEVD 641

RESULT 5  
HS71\_RAT  
ID HS71\_RAT STANDARD; PRT: 641 AA.  
AC 007439; P42853;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Heat shock 70 kDa protein 1/2 (HSP70.1/2).  
GN HSP70-1 AND HSP70-2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=94096443; PubMed=8273311;  
RA Lougo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,  
RT Massa S.M., Sharp F.R.;  
RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal  
RT and injured rat brain";  
RL J. Neurosci. Res. 36:325-335(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LEM.1W/GUN;  
RX MEDLINE=95012453; PubMed=7927536;  
RA Walter L., Rauh F., Guenther E.;  
RT "Comparative analysis of the three major histocompatibility complex-  
RT linked heat shock protein 70 (hsp70) genes of the rat";  
RL Immunogenetics 40:325-330(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=94368874; PubMed=8086479;  
RA Lisowska K., Krawczyk Z., Wlidlak W., Wolniczke P., Wisniewski J.;  
RT "Cloning, nucleotide sequence and expression of rat heat inducible  
RT hsp70 gene";  
RL Biochim. Biophys. Acta 1219:64-72(1994).  
RN [4]  
RP PREDICTED IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
RC PREDISTANT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
CC  
CC -1- INDUCTION: BY HEAT SHOCK.  
CC  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: L16764; AA17441.1; -;  
DR EMBL: X77208; CA54423.1; -;  
DR EMBL: X77207; CA54422.1; -;  
DR EMBL: X74271; CA52328.1; -;  
DR HSP: P08107; JH0;  
DR InterPro: IPR001023; Hsp70.  
DR Pfam: PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PRODOM: PD000089; HSP70; 1.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family.  
FT CONFLICT 71 KR -> NG (IN REF. 3).  
FT CONFLICT 72 D -> H (IN REF. 2 AND 3).  
FT CONFLICT 227

FT CONFLICT 408 408 G -> A (IN REF. 3).  
SQ SEQUENCE 641 AA; 70163 MM; D02D96751C868583 CRC64;  
Query Match 96.88; Score 3160; DB 1; Length 641;  
Best Local Similarity 96.48; Pred. No. 4.4e-168;  
Matches 618; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
QY 1 MAKAAATIDIGTGYSCGVFQHKGVETIANDQGRTPSYVAFDPTRRLGDAAKNQVA 60  
DB 1 MAKTAIGIDIGTYSVGVFQHKGVETIANDQGRTPSYVAFDPTRRLGDAAKNQVA 60  
QY 61 LNPQNTVADAKRLIGRKDPVVOVSDMKHMPVOVINDQDKRVQVSYGKTAFFPEIS 120  
DB 61 LNPQNTVADAKRLIGRKDPVVOVSDMKHMPVOVINDQDKRVQVSYGKTAFFPEIS 120  
QY 121 SMVLTRKMEIAEAYLVGVTNAVITVPAYFNDQKQATKADGAVIAGLVRLINEPTAA 180  
DB 121 SMVLTRKMEIAEAYLVGVTNAVITVPAYFNDQKQATKADGAVIAGLVRLINEPTAA 180  
QY 181 IAYGIDRTGKGERNVLTIDLGGFQDVSIITIDGIFEVKATAGDTHLGGDFQRLVNH 240  
DB 181 IAYGIDRTGKGERNVLTIDLGGFQDVSIITIDGIFEVKATAGDTHLGGDFQRLVNH 240  
QY 241 FVEEFKRRKKDISONKRAVRLRTACERAKRTLSSTQASLEIDSLEFEGIDFTYSITRA 300  
DB 241 FVEEFKRRKKDISONKRAVRLRTACERAKRTLSSTQASLEIDSLEFEGIDFTYSITRA 300  
QY 301 RFEEICSDLFESTLEPVEKALDAKDAKQIHDVLVVGSTRIPKVKRLDQFENGRLN 360  
DB 301 RFEEICSDLFESTLEPVEKALDAKDAKQIHDVLVVGSTRIPKVKRLDQFENGRLN 360  
QY 361 KSINDEAVAAQAQVAAIILMGDSENVODILLDVAFLSIGLEAGVMAALKRNSFI 420  
DB 361 KSINDEAVAAQAQVAAIILMGDSENVODILLDVAFLSIGLEAGVMAALKRNSFI 420  
QY 421 PTQQTQITTTSDNPGVLIQVYEGERAMTKDNMLGFELSGLEPPARGVPOIEVTDI 480  
DB 421 PTQQTQITTTSDNPGVLIQVYEGERAMTKDNMLGFELSGLEPPARGVPOIEVTDI 480  
QY 481 DANGILNATADKSTGKANKITITNDKGRLSKEETERNVOEAKYKADEVORERVAKN 540  
DB 481 DANGILNATADKSTGKANKITITNDKGRLSKEETERNVOEAKYKADEVORERVAKN 540  
QY 541 ALESTAFNMKSAVEDEGKIGKISEADKKVLDKCOEVSIMDANLAKDEFEHKKLE 600  
DB 541 ALESTAFNMKSAVEDEGKIGKISEADKKVLDKCOEVSIMDANLAKDEFEHKKLE 600  
QY 601 QVCNPTIISGLYQAGGPGGFGAOGPRGSGSGPTIEVD 641  
DB 601 QVCNPTIISGLYQAGGPGGFGAOGPRGSGSGPTIEVD 641  
RESULT 6  
HS71\_CERAE  
ID HS71\_CERAE STANDARD; PRT: 638 AA.  
AC Q28222;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DE Heat shock 70 kDa protein 1.  
GN HSPA1.  
OS Cercopithecus aethiops (Green monkey) (Givet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=95080396; PubMed=7988690;  
RA Saints I., Angelidis C., Pagoulatos G., Lazaridis I.;  
RT "The hsc70 gene which is slightly induced by heat is the main virus  
inducible member of the hsp70 gene family";

RL EBS Lett. 355:282-286(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
 CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
 CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
 CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
 CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
 CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
 CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING  
 CC STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X70684; CA50019.1; -  
 DR HSSP: P08107; IHO.  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR ProDom: PD000089; Hsp70; 1.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW ATP-binding; Chaperone; Heat shock; Multigene family.  
 SQ SEQUENCE 638 AA; 69920 MW; D55076A0FBA6B3 CRC64;

Query Match 96.5%; Score 3148.5; DB 1; Length 638;  
 Best local similarity 97.8%; Pred. No. 1.9e-167;  
 Matches 627; Conservative 1; Mismatches 10; Indels 3; Gaps 3;

QY 1 MAAAAAIGDLCGTYSCVGFQHGKVEITANDGNGRTTPEYVAFDTETRLIGAAKNOVA 60  
 DB 1 MAAAAAIGDLCGTYSCVGFQHGKVEITANDGNGRTTPEYVAFDTETRLIGAAKNOVA 60  
 QY 61 LNPONTVFDAKRLIGKRFQGVVQSDMKHMPFQVINDGDKPKQVQSKGTAKAYPEIS 120  
 DB 61 LNPONTVFDAKRLIGKRFQGVVQSDMKHMPFQVINDGDKPKQVQSKGTAKAYPEIS 120  
 QY 121 SMVLTAKKEIAEAYLYGYPYNAVITVPAYFNDQROATKDAGVIAGLNVLRITNEPTAA 180  
 DB 121 SMVLTAKKEIAEADLGYPYNAVITVPAYFNDQROATKDAGVIAGLNVLRITNEPT 179  
 QY 181 IAVGLDRTGGERNVLIPLDGGTFPDVSIITIDGIFEVKATAGDTHLGEDDNRNVN 240  
 DB 181 IAVGLDRTGGERNVLIPLDGGTFPDVSIITIDGIFEVKATAGDTHLGEDDNRNVN 240  
 QY 241 FVEEFKRRKKKDISSONKRAVRRLTACERAKRPTLSSTQASLEIDSLFEGIDYTSITRA 300  
 DB 241 FVEEFKRRKKKDISSONKRAVRRLTACERAKRPTLSSTQASLEIDSLFEGIDYTSITRA 300  
 QY 301 RFEELCSDLFIRSTLEPEVAKALDRAKQIHDLVLVGGSTRIPKYQKLLQDFENGRLN 360  
 DB 301 RFEELCSDLFIRSTLEPEVAKALDRAKQIHDLVLVGGSTRIPKYQKLLQDFENGRLN 360  
 QY 361 KSTNPDEAVAYGAAYAAIIMGKSENVODLLDLVAPLSLGIFETAGGVATALKRNSTI 420  
 DB 361 KSTNPDEAVAYGAAYAAIIMGKSENVODLLDLVAPLSLGIFETAGGVATALKRNSTI 420  
 QY 421 PKKOTQIFTTYSNQGVLIOVEGERAMTKDNNLGRFLSGIPAPRGVPOIEVTFDI 480  
 DB 421 PKKOTQIFTTYSNQGVLIOVEGERAMTKDNNLGRFLSGIPAPRGVPOIEVTFDI 480  
 QY 481 DANGILNVATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYAEDVEQREVSAN 540  
 DB 481 DANGILNVATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYAEDVEQREVSAN 540

DB 478 DANGILNVATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYAEDVEQREVSAN 537  
 QY 541 ALESYAFNNKSAVEDGLGKISEADKKRYVLDKCOEIVSLMANTLAERDEPFHKKRELE 600  
 DB 538 ALESYAFNNKSAVEDGLGKISEADKKRYVLDKCOEIVSLMANTLAERDEPFHKKRELE 597  
 QY 601 QVCNPIISGLYGAGCPGPGFAGQCPKGSQSGPTIEEVD 641  
 DB 598 QVCNPIISGLYGAGCPGPGFAGQCPKGSQSGPTIEEVD 638

RESULT 7  
 ID HS71.MOUSE STANDARD; PRT; 641 AA.  
 AC P17879; 061689;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN HSPAL OR HSP70A1 OR HSP70-1 OR HCP70.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90236310; PubMed=2332169;  
 RA Hunt C., Calderwood S.;  
 RT "Characterization and sequence of a mouse hsp70 gene and its  
 RT expression in mouse cell lines.";  
 RL Gene 87:199-204(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94357449; PubMed=8076831;  
 RA Perry M.D., Aujame L., Shtang S., Moran L.A.;  
 RT "Structure and expression of an inducible HSP70-encoding gene from  
 RT Mus musculus.";  
 RL Gene 146:273-278(1994).

-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M35021; AAA37864.1; -  
 DR EMBL: M76613; AAA57233.1; -  
 DR PIR: JH0095; JH0095.  
 DR HSSP: P08107; IHO.  
 DR MGD: MGI:99517; Hsp70-1.  
 DR InterPro: IPR001023; Hsp70.  
 DR Pfam: PF00012; HSP70\_1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR ProDom: PD000089; Hsp70; 1.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW ATP-binding; Chaperone; Heat shock; Multigene family.  
 FT CONFLICT 342 342 A -> R (IN REF. 1).  
 FT CONFLICT 627 627 P -> PP (IN REF. 1).



```

QY 422 TKQOIFTTYSNDQPGVLIQVYEGERAMTKDNLLGFEELSGIPAPRGVPOLEVTEDID 481
DB 424 PKQOIFTTYSNDQPGVLIQVYEGERAMTKDNLLGFEELDTGIPAPRGVPOLEVTEDID 483
QY 482 ANGLIANTADKSTGKANKTTITNDKGRLSKEEIERMVOAEKYYKADEVQREVSAKNA 541
DB 484 ANGLIANTADKSTGKANKTTITNDKGRLSKEEIERMVOAEKYYKADEVQREKIAAKNA 543
QY 542 LEEYAFNMKSAVDEGLKGIISADKKKVVLDKCOEVIISMDANTLAEKDEFEHKKRELEQ 601
DB 544 LEEYAFNMKSAVDEGLKGIISADKKKVVLDKCOEVIISMDANTLAEKDEFEHKKRELEQ 603
QY 602 VCNPIISGLVQAGGPPGGFGAOGPKGSGS-----SGPTIEVD 641
DB 604 MCBPIITKLYG-----GCTGPACGTGYVGRPATGPTIEVD 641

RESULT 9
HST7_MOUSE
ID HST7_MOUSE STANDARD; PRT: 641 AA.
AC P16627; 061693;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heat shock 70 kDa-like protein 1.
GN HSP70. OR HSC70T.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90147735; PubMed=2302214;
RA Matsumoto M., Fujimoto H.;
RT "Cloning of a hsp70-related gene expressed in mouse spermatids.";
RL Biochem. Biophys. Res. Commun. 166:43-49(1990).
RN (2)
RP REVISIONS.
RA Fujimoto H.;
RL Submitted (XX-1995) to the EMBL/Genbank/DBD databases.
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=94299288; PubMed=8026864;
RA Snook M., Olavesen M.G., van Vugt H., Milner C.M., Teuscher C.,
RA Campbell R.D.;
RT "Coding sequences and levels of expression of Hsc70t are identical in
RT mice with different Orch-1 alleles.";
RL Immunogenetics 40:159-162(1994).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SPERMATIDS.
CC -1- DEVELOPMENTAL STAGE: SPECIFICALLY EXPRESSED IN POSTMEIOTIC PHASES
CC OF SPERMATOGENESIS.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: M32218; AAA74906.1; -
DR EMBL: L27086; AAA59362.1; -
DR PIR: A34041; A34041.
DR HSSP: P08107; IHDJ.
DR MGD: MG196231; HSP70.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70.1
DR PRINTS: PRO0301; HEATSHOCK70.
DR PRODOM: PD000089; HSP70.1.
DR PROSITE: PS00297; HSP70_1; 1.

```

```

DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family; Spermatogenesis.
FT CONFLICT 634 634 D -> G (IN REF. 3).
SQ SEQUENCE 641 AA; 70695 MW; 3BCA15217803BC2A CRC64;

Query Match
Best Local Similarity 88.5%; Score 2887; DB 1; Length 641;
Matches 569; Conservative 32; Mismatches 36; Indels 2; Gaps 2;

QY 3 KAAIIGIDIGTYSQGVQVQHGKVELIANDQGRTPSYAFPTDRLLIGDAKNVAIN 62
DB 5 KGMATIGIDIGTYSQGVQVQHGKVELIANDQGRTPSYAFPTDRLLIGDAKNVAIN 64
QY 63 PONTVFDAKRLIRKRGDPVQSDMKHMPFOVINDDCKPRQVQSYGKTAFFPEISSM 122
DB 65 PONTVFDAKRLIRKRGDPVQSDMKHMPFOVINDDCKPRQVQSYGKTAFFPEISSM 124
QY 123 VLTFRKEIAEAYLGYPVTNAVITVPAYFNDQQRATKDAVIALNVLRIINEPTAAIA 182
DB 125 VLTFRKEIAEAYLGYPVTNAVITVPAYFNDQQRATKDAVIALNVLRIINEPTAAIA 184
QY 183 YGLDRTGKGERNVLIIDLGSGTQVSIILITDQIIEFKATAGTHLIGEDFQNRILYNHV 242
DB 185 YGLDRTGKGERNVLIIDLGSGTQVSIILITDQIIEFKATAGTHLIGEDFQNRILYNHV 244
QY 243 EEFKRRHKKDISONKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFVTSIRAF 302
DB 245 EEFKRRHKKDISONKRAVRRLTACERAKRTLSSSTQASLEIDSLFEGIDFVTSIRAF 304
QY 303 EELCSDFRSTLEPVEKALRDANKIHDVLYVGSSTRIPKVKLIDFENGRLNKS 362
DB 305 EELCSDFRSTLEPVEKALRDANKIHDVLYVGSSTRIPKVKLIDFENGRLNKS 364
QY 363 INPDEAVAYGAQAAILMGDKSENVODLLLDVAFLSLGLETAGVYVALLKRNSTIPT 422
DB 365 INPDEAVAYGAQAAILMGDKSENVODLLLDVAFLSLGLETAGVYVALLKRNSTIPT 424
QY 423 KQOIFTTYSNDQPGVLIQVYEGERAMTKDNLLGFEELSGIPAPRGVPOLEVTEDID 482
DB 425 KQOIFTTYSNDQPGVLIQVYEGERAMTKDNLLGFEELDTGIPAPRGVPOLEVTEDID 484
QY 483 NGILNVTATDKSTGKANKTTITNDKGRLSKEEIERMVOAEKYYKADEVQREVSAKNA 542
DB 485 NGILNVTATDKSTGKANKTTITNDKGRLSKEEIERMVOAEKYYKADEVQREKIAAKNA 544
QY 543 ESYAFNMKSAVDEGLKGIISADKKKVVLDKCOEVIISMDANTLAEKDEFEHKKRELEQ 602
DB 545 ESYAFNMKSAVDEGLKGIISADKKKVVLDKCOEVIISMDANTLAEKDEFEHKKRELEQ 604
QY 603 CNPIISGLVQAGGPPGGFGAOGPKGSGSPTIEVD 641
DB 605 CNPIITKLYG-----GCTGPACGTGYVGRPATGPTIEVD 641

RESULT 10
HST7_RAT
ID HST7_RAT STANDARD; PRT: 641 AA.
AC P55063;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Heat shock 70 kDa protein 3 (HSP70.3).
GN HSP70-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=LEW.1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter L., Rauch F., Guenther E.;

```

\*Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.\*;  
 RT Immunogenetics 40:325-330(1994)  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X77209; CA54424.1; .  
 DR HSSP; P08107; 1HJO.  
 DR InterPro; IPR001023; Hsp70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PRODOM; PD000089; HSP70; 1.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family.  
 KW SEQUENCE 641 AA; 70549 MW; 8C77AA9FD98B9252 CRC64;

Query Match 88.3%; Score 2882; DB 1; Length 641;  
 Best Local Similarity 88.6%; Pred. No. 1,le-152;

Matches 569; Conservative 32; Mismatches 33; Indels 8; Gaps 3;

QY 3 KAAALIGDITGVVGVFGHKGVEIINDDGNRTPEVAFPTDTERLIGDAKQVAVLN 62  
 DB 5 KGMALIGDITGVVGVFGHKGVEIINDDGNRTPEVAFPTDTERLIGDAKQVAVLN 64  
 QY 63 PONTVFDAKRLIGKFGCPVVOQSDMKHMPFOVINDGDKPKVOVSXKGTAKAFPEISIM 122  
 DB 65 PONTVFDAKRLIGKFGCPVVOQSDMKHMPFOVINDGDKPKVOVSXKGTAKAFPEISIM 124  
 QY 123 VLTAKKEIAEAYLGYPVNAVITVPAYFNDQSORATKDAGVYAGLNLRIINEPTAAIA 182  
 DB 125 VLTAKKEIAEAYLGYPVNAVITVPAYFNDQSORATKDAGVYAGLNLRIINEPTAAIA 184  
 QY 183 YGIDRTGGERNNVLFIDGGTTPVYSITITDDGTFEVATAGDTHLGGEDFDNRLVNHFV 242  
 DB 185 YGIDRTGGERNNVLFIDGGTTPVYSITITDDGTFEVATAGDTHLGGEDFDNRLVNHFV 244  
 QY 243 EEFKRRKKKDISSONKRAVRRLTACERAKRTLSSTOASLEDSLFEGLIDFTSTTRARF 302  
 DB 245 EEFKRRKKKDISSONKRAVRRLTACERAKRTLSSTOASLEDSLFEGLIDFTSTTRARF 304  
 QY 303 EELCSDLRSTLPEYKALRDADKQIHDVLVVGSTRIIPKVOYKLLQDFNGRDLNKS 362  
 DB 305 EELCADLFRGLTLEPEYKALRDADKQIHDVLVVGSTRIIPKVOYKLLQDFNGRDLNKS 364  
 QY 363 INPBEAVAYGAQAAILMGDKSENVQDILLDAVAPLSLGLETAGCWTALIKRSTIPT 422  
 DB 365 INPBEAVAYGAQAAILMGDKSENVQDILLDAVAPLSLGLETAGCWTALIKRSTIPT 424  
 QY 423 KOTQIFTTYSNOPGVLLQVEGERAMTKDNNILGRFELSGIPPAKGVPOTEVYFDIDA 482  
 DB 425 KOTQIFTTYSNOPGVLLQVEGERAMTKDNNILGRFELSGIPPAKGVPOTEVYFDIDA 484  
 QY 483 NGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOAEKRYKAEDVQREVSAAKAL 542  
 DB 485 NGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOAEKRYKAEDVQREVSAAKAL 544

QY 543 ESYAFNMKSAYEDGELGKISEADKKRVLKDCQEVISLWANTLAKDEFEKRRKLEQV 602  
 DB 545 ESYAFNMKSAYEDGELGKISEADKKRVLKDCQEVISLWANTLAKDEFEKRRKLEQV 604  
 QY 603 CNPIITKLYQ-GAGCP--GPGFGAOCGPKGSGSGPTTEEVD 641  
 DB 605 CNPIITKLYQSGCGPGTCAPG-----YTPGARARGTTEEVD 641

RESULT 11  
 HSC7\_MOUSE STANDARD: PRT; 646 AA.  
 AC P08109; P12225; Q62373; Q62374; Q62375;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Heat shock cognate 71 kDa protein.  
 GN HSPA8 OR HSC70 OR HSC73.  
 OS Mus musculus (Mouse), and  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090, 10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Rat;  
 RX MEDLINE=87246537; PubMed=3595567;  
 RA "Sorgner P. K., Pelham H. R. B.;  
 RT "Cloning and expression of a gene encoding hsc73, the major hsp70-like  
 RT protein in unstressed rat cells.";  
 RL EMBO J. 6:993-998(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Rat;  
 RX MEDLINE=86310827; PubMed=3939319;  
 RA "O'Malley K., Mauron A., Barchas J.D., Kedes L.;  
 RT "Constitutively expressed rat mRNA encoding a 70-kilodalton heat-  
 RT shock-like protein.";  
 RL Mol. Cell. Biol. 5:3476-3483(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Mouse; STRAIN=129; TISSUE=Mammary gland;  
 RX Soulier S., Ylloite J.-L., L'Huillier P.-J., Mercier J.-C.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Mouse;  
 RX MEDLINE=88055872; PubMed=3334718;  
 RA "Gleibel L.B., Dworniczak B.P., Baulz E.K.F.;  
 RT "Developmental regulation of a constitutively expressed mouse mRNA  
 RT encoding a 72-kDa heat shock-like protein.";  
 RL Dev. Biol. 125:200-207(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Mouse; STRAIN=129;  
 RA Hunt C.R.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 333-383; 438-452 AND 580-587 FROM N.A.  
 RC SPECIES-Mouse;  
 RX MEDLINE=91067440; PubMed=2251119;  
 RA Liu J., Maxwell E.S.;  
 RT "Mouse U1A snRNA is encoded in an intron of the mouse cognate hsc70  
 RT heat shock gene.";  
 RL Nucleic Acids Res. 18:6565-6571(1990).  
 RN [7]  
 RP STRUCTURE BY NMR OF 385-543.  
 RC SPECIES-Rat;  
 RX MEDLINE=99303702; PubMed=10373374;  
 RA Morshauer R.C., Hu W., Wang H., Pang Y., Flynn G.C.,  
 RA Zuiderweg E.R.P.;  
 RT "High-resolution solution structure of the 18 kDa substrate-binding

RT domain of the mammalian chaperone protein Hsc70." ;  
 RL J. Mol. Biol. 289:1387-1403(1999).  
 CC -1- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; Y00054; CAA68265.1; -  
 DR EMBL; M11942; AAA41354.1; -  
 DR EMBL; U27129; AAC52836.1; -  
 DR EMBL; M19141; AAA37869.1; -  
 DR EMBL; U73744; AAB18391.1; -  
 DR EMBL; X54401; CAA38267.1; -  
 DR EMBL; X54402; CAA38268.1; -  
 DR EMBL; X54403; CAA38269.1; -  
 DR PIR; S07197; S07197.  
 DR PIR; A45935; A45935.  
 DR PDB; 1CKR; 30-APR-99.  
 DR SWISS-2DPAGE; P08109; MOOSE.  
 DR MGD; MGI:105384; HspA8.  
 DR InterPro; IPR001023; Hsp70.  
 DR Pfam; PF00012; Hsp70.1  
 DR PRINTS; PRO0301; HEATSHOCK70.  
 DR PRODOM; PD000089; Hsp70.1.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW ATP-binding; Heat shock; Multigene family; 3D-structure.  
 FT CONFLICT 428 428 F -> L (IN REF. 4 AND 5).  
 SQ SEQUENCE 646 AA; 70871 MW; 03A27B30EC076ED CRC64;  
 Query Match 87.7%; Score 2862.5; DB 1; Length 646;  
 Best Local Similarity 85.8%; Pred. No. 1.4e-151;  
 Matches 554; Conservative 47; Mismatches 40; Indels 5; Gaps 3;  
 QY 1 MAAAAIGDGLGTTSCVGFQHGKVEIIANDOGNRTTSPYVAFPTTERLIGAAKNQVA 60  
 DB 1 MSKGPVAGIDLGTTSCVGFQHGKVEIIANDOGNRTTSPYVAFPTTERLIGAAKNQVA 60  
 QY 61 LNKONTVFDAKRLIGRFGPPVQSDMKHMPFOVINDGDKPKOVQSKGTAFYPEETS 120  
 DB 61 MNPNTNVFDAKRLIGRFGPPVQSDMKHMPFOVINDGDKPKOVQSKGTAFYPEETS 120  
 QY 121 SMVLTKMKEIAEAYLGYPVTNAVITPAYFNDGSRQATKDAGYIAGINVLRIINEPTAA 180  
 DB 121 SMVLTKMKEIAEAYLGKTVNAVITPAYFNDGSRQATKDAGYIAGINVLRIINEPTAA 180  
 QY 181 IANGLDRTGGERNVLIFFDGGSTFDVSIITIDGIFEVKATAGDTHLGEDDNLVNH 240  
 DB 181 IANGLDRTGGERNVLIFFDGGSTFDVSIITIDGIFEVKATAGDTHLGEDDNLVNH 240  
 QY 241 FVEEFKRRKKKIDISOKKRAVRRLRTACERAKRTLSSTQSLFIDSLFEGIDFTYSITRA 300  
 DB 241 FVEEFKRRKKKIDISOKKRAVRRLRTACERAKRTLSSTQSLFIDSLFEGIDFTYSITRA 300  
 QY 301 REBELCSLFRSTLEPEYERKALRDALDKAQIHDVLVVGSTRIIPKYOKLIDDFENGRDLN 360  
 DB 301 REBELCSLFRSTLEPEYERKALRDALDKAQIHDVLVVGSTRIIPKYOKLIDDFENGRDLN 360  
 QY 361 KSIINPEAAVYGAAYAAIIMGKSENVODLLDVAPISLGLETAGCVTALIKRNSTI 420  
 DB 361 KSIINPEAAVYGAAYAAIIMGKSENVODLLDVAPISLGLETAGCVTALIKRNSTI 420  
 QY 421 PTKORQIFPTTYSNONGVLIOVEGERAMTKNNLIGRFLSGIIPAPRGVQIETFPDI 480  
 DB 421 PTKORQIFPTTYSNONGVLIOVEGERAMTKNNLIGRFLSGIIPAPRGVQIETFPDI 480

QY 481 DANGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYAEDEVORERVSAKN 540  
 DB 481 DANGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYAEDEVORERVSAKN 540  
 QY 541 ALESYAFNMKSAVEDGGLKGISEADKKRYLDKQCVISVMDANTLAEDFEERHKKKE 600  
 DB 541 SLESYAFNMKSAVEDGGLKGISEADKKRYLDKQCVISVMDANTLAEDFEERHKKKE 600  
 QY 601 QVNCPIITTKLYGSAGSGMFGMGGFPGGAPSPSGASSGPTIEYD 641  
 DB 601 QVNCPIITTKLYGSAGSGMFGMGGFPGGAPSPSGASSGPTIEYD 641  
 RESULT 12  
 HS7C\_HUMAN  
 ID HS7C\_HUMAN STANDARD; PRT; 646 AA.  
 AC P11142;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Heat shock cognate 71 kDa protein.  
 GN HSPA8 OR HSPA10 OR HSC70 OR HSP73.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=67259994; PubMed=3037489;  
 RA Dworniczak B.P., Mirault M.-E.;  
 RT "Structure and expression of a human gene coding for a 71 kd heat  
 RT shock 'cognate' protein." ;  
 RL Nucleic Acids Res. 15:5181-5197(1987).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RL Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP MEDLINE=93162043; PubMed=1286667;  
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
 RA Vandekerckhove J.;  
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
 RT protein database of normal human epidermal keratinocytes." ;  
 RL Electrophoresis 13:960-969(1992).  
 RN [4]  
 RP SEQUENCE OF 77-86; 221-236 AND 302-311.  
 RX MEDLINE=96311348; PubMed=8713105;  
 RA Egerton M., Moritz R.L., Drucker B., Kelse A., Simpson R.J.;  
 RA "Identification of the 70kd heat shock cognate protein (hsc70) and  
 RT alpha-actinin-1 as novel phosphotyrosine-containing proteins in T  
 RT lymphocytes." ;  
 RL Biochem. Biophys. Res. Commun. 224:666-674(1996).  
 CC -1- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; Y00371; CAA68445.1; -  
 DR EMBL; BC016179; AAH16179.1; -  
 DR PIR; A27077; A27077.  
 DR HSSP; P19120; IATR.  
 DR SWISS-2DPAGE; P11142; HUMAN.  
 DR Aairnus/Chent-2DPAGE; 6504; IEF.  
 DR PHCI-2DPAGE; P11142; -  
 DR HSC-2DPAGE; P11142; HUMAN.



DR Genew; HGNC:5241; HSPAB.  
 DR MIM; 600816; -  
 DR InterPro; IPR001023; Hsp70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR ProDom; PD000089; Hsp70; 1.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR ATP-binding; Heat shock; Multigene family.  
 KW SEQUENCE 646 AA; 70898 MW; 9AA27B210730670C CRC64;

Query Match 87.6%; Score 2859.5; DB 1; Length 646;  
 Best Local Similarity 85.6%; Pred. No. 2e-151;  
 Matches 553; Conservative 48; Mismatches 40; Indels 5; Gaps 3;

QY 1 MAKAAIGIDGTYTSCGVFQHGKVEIIANDQGNRTTSSVAFDTERTLIGDAKNQVA 60  
 DB 1 MSKPAVAGIDGTYTSCGVFQHGKVEIIANDQGNRTTSSVAFDTERTLIGDAKNQVA 60  
 QY 61 LNPQTVFADARLIGRKRGDPVQSDMKHMPFOVINDDKRKQVSYGKTKAFYPEIS 120  
 DB 61 NMPITVFADARLIGRRPDDAVQSDMKHMPVNDGRRKQVYEGTKSPFPEVS 120  
 QY 121 SMVLTKMEIEAYLGYPVNAVITVPAYFNDSPQATKDGAVIAGLVLRINEPTAA 180  
 DB 121 SMVLTKMEIEAYLGYPVNAVITVPAYFNDSPQATKDGAVIAGLVLRINEPTAA 180  
 QY 181 IAYGIDRTGKERNYLIFDLGGTFEVSILTDGIFEVKATAGDTHLGEDFDMRLVNH 240  
 DB 181 IAYGIDRTGKERNYLIFDLGGTFEVSILTDGIFEVKATAGDTHLGEDFDMRLVNH 240  
 QY 241 FVEERKRRHKKDIGNKRAVRLRACERAKRTLSSTQASLEIDSLFEGIDFTYSIRA 300  
 DB 241 FVEERKRRHKKDIGNKRAVRLRACERAKRTLSSTQASLEIDSLFEGIDFTYSIRA 300  
 QY 301 RFEELCSOLFSTLEPVEKALRDALDKAOLHDVLVGSSTRIPVOKLLODFNGRDLN 360  
 DB 301 RFEELCSOLFSTLEPVEKALRDALDKAOLHDVLVGSSTRIPVOKLLODFNGRDLN 360  
 QY 361 KSIINDEAVAGAAVQAAIIMGDKSENVODLLLDVAPLSIGLETAGGVMALIKRNTI 420  
 DB 361 KSIINDEAVAGAAVQAAIIMGDKSENVODLLLDVAPLSIGLETAGGVMALIKRNTI 420  
 QY 421 PTKQQTITTSNDQPGVLIQYSEERAMTKDNILRFEELSGIPAPRGVQITVTDI 480  
 DB 421 PTKQQTITTSNDQPGVLIQYSEERAMTKDNILRFEELSGIPAPRGVQITVTDI 480  
 QY 481 DANGILNTATDKSTGKANKITITNDKGRLSKEETIERMVOEAKKARDEVOREVSKN 540  
 DB 481 DANGILNTATDKSTGKANKITITNDKGRLSKEETIERMVOEAKKARDEVOREVSKN 540  
 QY 541 ALESYAFNMKSAVDEDEGLKISADKKRVLDCOEVIISWLDANTLADEFEHRRKELE 600  
 DB 541 ALESYAFNMKSAVDEDEGLKISADKKRVLDCOEVIISWLDANTLADEFEHRRKELE 600  
 QY 601 QVCNRTISGLVQAGG-PG--PGGF--GAQGRKGGSGSPTEEDV 641  
 DB 601 QVCNRTISGLVQAGG-PG--PGGF--GAQGRKGGSGSPTEEDV 641  
 QY 641 KVCNPIITKLYOSAGMGPMGPGPGGAGPAGSGASSGPTIEEDV 646  
 DB 641 KVCNPIITKLYOSAGMGPMGPGPGGAGPAGSGASSGPTIEEDV 646

RESULT 13  
 HS7C\_BOVIN  
 ID HS7C\_BOVIN STANDARD: PRT; 650 AA.  
 AC P19120;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Heat shock cognate 71 kDa protein.  
 GN HSPAB OR HSC70.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

CC Bovidae; Bovinae; Bos.  
 RX NCBI\_Taxid=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain cortex;  
 RX MEDLINE=91016866; PubMed=2216746;  
 RA Deluca-Flaherty C., McKay D.B.;  
 RT "Nucleotide sequence of the cDNA of a bovine 70 kDa heat shock cognate protein.";  
 RL Nucleic Acids Res. 18:5569-5569(1990).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1-385.  
 RX MEDLINE=90348961; PubMed=2143562;  
 RA Flaherty K.M., de Luca-Flaherty C., McKay D.B.;  
 RT "Three-dimensional structure of the ATPase fragment of a 70K heat-shock cognate protein.";  
 RL Nature 346:623-628(1990).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-385.  
 RX MEDLINE=94230372; PubMed=8175707;  
 RA Flaherty K.M., Wilbanks S.M., Deluca-Flaherty C., McKay D.B.;  
 RT "Structural basis of the 70-kDa heat shock cognate protein ATP hydrolytic activity. II. Structure of the active site with ADP or ATP bound to wild type and mutant ATPase fragment.";  
 RL J. Biol. Chem. 269:12899-12907(1994).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-385.  
 RX MEDLINE=96254532; PubMed=9585559;  
 RA Wilbanks S.M., McKay D.B.;  
 RT "Structural replacement of active site monovalent cations by the epsilon-amino group of lysine in the ATPase fragment of bovine Hsc70.";  
 RL Biochemistry 37:7456-7462(1998).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 1-381.  
 RX MEDLINE=99017893; PubMed=9799500;  
 RA Sousa M.C., McKay D.B.;  
 RT "The hydroxyl of the threonine 13 of the bovine 70-kDa heat shock cognate protein is essential for transducing the ATP-induced conformational change.";  
 RL Biochemistry 37:15392-15399(1998).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-381 OF MUTANTS.  
 RX MEDLINE=99379828; PubMed=10451379;  
 RA Johnson E.R., McKay D.B.;  
 RT "Mapping the role of active site residues for transducing an ATP-induced conformational change in the bovine 70-kDa heat shock cognate protein.";  
 RL Biochemistry 38:10823-10830(1999).  
 CC -1- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X53827; CA37823.1; -;  
 DR EMBL; X53335; CA37422.1; -;  
 DR PIR; S11456; S11456.  
 DR PDB; 3HSC; 10-JUL-95.  
 DR PDB; 1ATR; 30-APR-94.  
 DR PDB; 1ATS; 30-APR-94.  
 DR PDB; 1NGA; 31-AUG-94.  
 DR PDB; 1NGB; 31-AUG-94.  
 DR PDB; 1NGC; 31-AUG-94.  
 DR PDB; 1NGD; 31-AUG-94.  
 DR PDB; 1NGE; 31-AUG-94.  
 DR PDB; 1NGF; 31-AUG-94.  
 DR PDB; 1NGG; 31-AUG-94.

DR PDB; 1NGH; 31-AUG-94.  
DR PDB; 1NGI; 31-AUG-94.  
DR PDB; 1NGJ; 31-AUG-94.  
DR PDB; 1HPM; 31-JUL-95.  
DR PDB; 1KAX; 08-NOV-96.  
DR PDB; 1KAY; 08-NOV-96.  
DR PDB; 1KAZ; 08-NOV-96.  
DR PDB; 1BA0; 15-JUL-98.  
DR PDB; 1BA1; 15-JUL-98.  
DR PDB; 1BUP; 09-SEP-98.  
DR PDB; 2BUP; 16-SEP-98.  
DR PDB; 1QOM; 15-SEP-99.  
DR PDB; 1QON; 15-SEP-99.  
DR PDB; 1QOO; 15-SEP-99.  
DR InterPro; IPRO01023; Hsp70.  
DR Pfam; PF00012; Hsp70; 1.  
DR PRINTS; PRO0301; HEATSHOCK70.  
DR PRODOM; PD000089; Hsp70; 1.  
DR PROSITE; PS00297; Hsp70\_1; 1.  
DR PROSITE; PS00329; Hsp70\_2; 1.  
DR PROSITE; PS01036; Hsp70\_3; 1.  
KM ATP-binding; Heat shock; Multigene family; 3D-structure.  
FT STRAND 7 11  
FT STRAND 15 22  
FT TURN 23 24  
FT STRAND 25 28  
FT TURN 32 33  
FT STRAND 38 39  
FT STRAND 42 44  
FT STRAND 49 51  
FT TURN 52 52  
FT TURN 53 56  
FT TURN 57 61  
FT TURN 63 65  
FT STRAND 66 67  
FT TURN 70 72  
FT TURN 73 75  
FT TURN 78 79  
FT TURN 81 87  
FT TURN 88 89  
FT STRAND 93 97  
FT TURN 98 99  
FT STRAND 100 107  
FT TURN 108 109  
FT STRAND 110 114  
FT TURN 116 135  
FT STRAND 136 136  
FT STRAND 141 146  
FT TURN 148 149  
FT TURN 152 164  
FT TURN 165 166  
FT STRAND 168 174  
FT HELIX 175 182  
FT TURN 183 186  
FT STRAND 193 200  
FT STRAND 205 213  
FT TURN 214 215  
FT STRAND 216 225  
FT TURN 226 227  
FT HELIX 230 249  
FT TURN 254 255  
FT HELIX 257 274  
FT TURN 275 276  
FT STRAND 279 288  
FT TURN 289 290  
FT STRAND 291 298  
FT TURN 299 312  
FT TURN 313 313  
FT HELIX 314 324  
FT TURN 325 325  
FT HELIX 328 330  
FT STRAND 333 337  
FT HELIX 339 342

FT HELIX 344 353  
FT TURN 354 356  
FT STRAND 359 360  
FT TURN 365 367  
FT HELIX 368 379  
FT TURN 380 381  
SQ SEQUENCE 650 AA; 71239 MW; 5BEB36C2AF30493 CRC64;

Query Match 87.5%; Score 2853.5; DB 1; Length 650;  
Best Local Similarity 84.9%; Pred. No. 4,4e-151;  
Matches 552; Conservative 49; Mismatches 40; Indels 9; Gaps 3;

QY 1 MAAAAIGIDLGTTYSQVGVFQHGKVEIIANDQGNFTPSYVAFDTYERLIGDAKNQYA 60  
DB 1 MSKGPVAGIDLGTTYSQVGVFQHGKVEIIANDQGNFTPSYVAFDTYERLIGDAKNQYA 60  
QY 61 LNPQNTVPDAKRLIGKFPDVPVQSDMKHMPPOYINDGKPKVQVSYKETAFAFYEEIS 120  
DB 61 MNPNTVPDAKRLIGRFPDVAVQSDMKHMPVNVNDAGRPKVQVEYKGETSYFEYS 120  
QY 121 SMVLTAKKEIAEAYLGYPYTNVITVPAYENDSORQATDAGYIAGLNVLRINEPTAA 180  
DB 121 SMVLTAKKEIAEAYLGKTYTNVITVPAYENDSORQATDAGYIAGLNVLRINEPTAA 180  
QY 181 IAYGLDRTGKGERNVLIIPDLGGTFDVSILITDDGIFEYKATAGDTHLGGEFDNRNVH 240  
DB 181 IAYGLDKVGAERNVLIIPDLGGTFDVSILITDDGIFEYKATAGDTHLGGEFDNRNVH 240  
QY 241 FYEEFKRKHKDLSQKRRVRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300  
DB 241 FIAEFKRRKHKDISENKRVRRLRTACERAKRTLSSSTQASLEIDSLYEGIDFYTSITRA 300  
QY 301 RFEEICSDLFIRSTLEPVEKALRDAKLDKAOIHDLVYVGSTRIPKYQKLLDQFFNGRDIN 360  
DB 301 RFEEINADLFRTGLDPEVERALRDAKLDKQIHDYLVGSTRIPKYOQLDQFFNKEIN 360  
QY 361 KSTNPDEAVAYGAVOAAILMGDSENVODLLLDVAPLSIGLETAGVYWTALIKNSTI 420  
DB 361 KSTNPDEAVAYGAVOAAILISGDSENVODLLLDVTPSLIGTAGVYWTALIKNSTI 420  
QY 421 PTKOTQIFFTYSNORGVLIQVYEGERAMTKDNLLGRELISIPAPRGVPIEYTPDI 480  
DB 421 PTKOTQIFFTYSNORGVLIQVYEGERAMTKDNLLGRELISIPAPRGVPIEYTPDI 480  
QY 481 DANGILNVTATDSTGKANKITTTNDKGRLSKEIERMTOEAEKYAEDEVOREVRSAN 540  
DB 481 DANGILNVSADVSTGKREKITTNDKGRLSKEDIERMTOEAEKYAEDEKQRDKVSAN 540  
QY 541 ALESYAFNMKSAYEDELGKISEADKKVLDKQCEVISWLDANTLAERDEFEHKKLE 600  
DB 541 SLKSYAFNMKATVEDEKLGKINDEDEKILDKCNEIINWLDKNQTAEREFEHQELE 600  
QY 601 QVCNPIISGLYQAGG-----PGF--PGGF--GAQGPKGSGSGSPTEEVD 641  
DB 601 KYCNPILITKLYQAGGPGMGPGMGPGGPGGAPPSGASGSPTEEVD 650

RESULT 14  
HSTC\_CRIGR STANDARD; PRT; 646 AA.  
ID HSTC\_CRIGR AC P19378;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Heat shock cognate 71 kDa protein.  
GN HSPA8 OR HSC70.  
OS Cricetulus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetulus.  
OX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE FROM N.A.

```

RX MEDLINE=90377205; PubMed=1975944;
RA. Ahmad S., Ahuja R., Vanner T.J., Gupta R.S.;
RT Identification of a protein altered in mutants resistant to
RT microtubule inhibitors as a member of the major heat shock protein
RT (hsp70) family.
RL Mol. Cell. Biol. 10:5160-5165(1990).
CC -1- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34561; AAA6991.1; -.
DR PIR; A35922; A35922.
DR HSSP; P08109; 1CKR.
DR InterPro: IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PRO0301; HEATSHOCK70.
DR PRODOM; PD000089; HSP70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW SEQUENCE 646 AA; 70805 MW; FC65A2DC5095AD1C CRC64;

Query Match      87.1%; Score 2843.5; DB 1; Length 646;
Best Local Similarity 85.3%; Pred. No. 1.6e-150;
Matches 551; Conservative 47; Mismatches 43; Indels 5; Gaps 3;

OY 1 MAKAAAIIDIGTGYSCGVGFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAAKNOVA 60
DB 1 MSKGAVVVIDIGTGYSCGVGFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAAKNOVA 60
OY 61 LNPQVTVDAKRLIGRGDPPVVOVSDMKHMPVOVINDGDKPRVOVSYKGETAFPEEIS 120
DB 61 MNPVTVPDAKRLIGRRFDVAVVSDMKHMPVVDAGRPVOVYVEYKGAHSFPEEVS 120
OY 121 SWVLTKMKEIEAVALGYPTNAVITVPAYFNDORQATFACVIGLVNLRINEPTAA 180
DB 121 SWVLTKMKEIEAVALGYPTNAVITVPAYFNDORQATFACVIGLVNLRINEPTAA 180
OY 181 IAYGLDRTGKGERNVLIEDLGSGTFDVSILITIDGIFEVKATAGDTHLGGEDEDNRLVNH 240
DB 181 IAYGLDRTGKGERNVLIEDLGSGTFDVSILITIDGIFEVKATAGDTHLGGEDEDNRLVNH 240
OY 241 FVEERKRRKHKDI SONKRAVRRLRTACERAKRTLSSTQASLEIDSLEFGIDFYSITRA 300
DB 241 FVEERKRRKHKDI SONKRAVRRLRTACERAKRTLSSTQASLEIDSLEFGIDFYSITRA 300
OY 301 FFAEERKRDKNKDI SENKRAVRRLRTACERAKRTLSSTQASLEIDSLEFGIDFYSITRA 300
DB 301 FFAEERKRDKNKDI SENKRAVRRLRTACERAKRTLSSTQASLEIDSLEFGIDFYSITRA 300
OY 360 REEELCSDFLEFSTLEPVEKALDKADLKAQIHDVLVGGSTPIPVYOKLLODFEFGRODN 360
DB 360 REEELCSDFLEFSTLEPVEKALDKADLKAQIHDVLVGGSTPIPVYOKLLODFEFGRODN 360
OY 360 REEELNADLFKRTLDLPEVEKALDKADLKAQIHDVLVGGSTPIPVYOKLLODFEFGRODN 360
DB 360 REEELNADLFKRTLDLPEVEKALDKADLKAQIHDVLVGGSTPIPVYOKLLODFEFGRODN 360
OY 420 KSIINDEAVAYGAOVAALILMGDKSENVODLLLDVAPLSLIGLETAGVYMLIRKNSSTI 420
DB 420 KSIINDEAVAYGAOVAALILMGDKSENVODLLLDVAPLSLIGLETAGVYMLIRKNSSTI 420
OY 480 PTKOQITFTTYSNDOPGVLIQYEGEERAMTKDNNLLGKKEELGIPAPRGVQOIEYTFPI 480
DB 480 PTKOQITFTTYSNDOPGVLIQYEGEERAMTKDNNLLGKKEELGIPAPRGVQOIEYTFPI 480
OY 540 DANGILNTATDSTGKANKITITNDKGRLSKEEIERMVOAEKYKADEYQORERYSAN 540
DB 540 DANGILNTATDSTGKANKITITNDKGRLSKEEIERMVOAEKYKADEYQORERYSAN 540
OY 540 DANGILNTATDSTGKANKITITNDKGRLSKEEIERMVOAEKYKADEYQORERYSAN 540
DB 540 DANGILNTATDSTGKANKITITNDKGRLSKEEIERMVOAEKYKADEYQORERYSAN 540
OY 600 ALESTYAFNMKSAVEDEGIGKISEADKKKKVLDKCOEVI SWLDANTLAEKDEEHRKKELE 600
DB 600 ALESTYAFNMKSAVEDEGIGKISEADKKKKVLDKCOEVI SWLDANTLAEKDEEHRKKELE 600
OY 600 ALESTYAFNMKSAVEDEGIGKISEADKKKKVLDKCOEVI SWLDANTLAEKDEEHRKKELE 600
DB 600 ALESTYAFNMKSAVEDEGIGKISEADKKKKVLDKCOEVI SWLDANTLAEKDEEHRKKELE 600

```

```

OY 601 OVCNPIITSLGYGAGG-PG--PGGF--GAQPGKSGSGPTREEVD 641
DB 601 KVCNPIITSLKLYOSAGGMFGMFGGFPGGGAPPSGGAASSGPTREEVD 646

RESULT 15
HS70_XENLA STANDARD; PRT; 647 AA.
ID HS70_XENLA
AC P02827;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 01-JUL-1993 (rel. 26, Last annotation update)
DE Heat shock 70 kDa protein (HSP70).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85076567; PubMed=6510409;
RX Bienz M.;
RT "Xenopus hsp 70 genes are constitutively expressed in injected
RT oocytes."
RL EMBO J. 3:2477-2483(1984).
RN [2]
RP SEQUENCE OF 81-120 FROM N.A.
RA MEDLINE=84221917; PubMed=6203112;
RX Bienz M.;
RT "Developmental control of the heat shock response in Xenopus."
RL Proc. Natl. Acad. Sci. U.S.A. 81:3138-3142(1984).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01102; CAA25576.1; -.
DR EMBL; K02307; AAA49759.1; -.
DR PIR; A03310; HHXL70.
DR HSSP; P08107; 1H00.
DR InterPro: IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PRO0301; HEATSHOCK70.
DR PRODOM; PD000089; HSP70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 647 AA; 70915 MW; 33AFA9BBFA2FE23 CRC64;

Query Match      86.9%; Score 2835.5; DB 1; Length 647;
Best Local Similarity 85.3%; Pred. No. 4.3e-150;
Matches 551; Conservative 51; Mismatches 35; Indels 9; Gaps 4;

OY 3 KAAAGIDIGTGYSCGVGFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNOVALN 62
DB 1 KAAAGIDIGTGYSCGVGFQHGKVEIANDQGNRTTPSYAFTDTERLIGDAKNOVALN 62
OY 63 PONTVPDAKRLIGRGDPPVVOVSDMKHMPVOVINDGDKPRVOVSYKGETAFPEEISSM 122
DB 63 PONTVPDAKRLIGRGDPPVVOVSDMKHMPVOVINDGDKPRVOVSYKGETAFPEEISSM 122
OY 123 VLTAKKEIEAVALGYPTNAVITVPAYFNDORQATKADGVLAVNLRINEPTAAATA 182
DB 123 VLTAKKEIEAVALGYPTNAVITVPAYFNDORQATKADGVLAVNLRINEPTAAATA 182
OY 182 VLTAKKEIEAVALGYPTNAVITVPAYFNDORQATKADGVLAVNLRINEPTAAATA 182
DB 182 VLTAKKEIEAVALGYPTNAVITVPAYFNDORQATKADGVLAVNLRINEPTAAATA 182
OY 242 YGLDRTGKGERNVLIEDLGSGTFDVSILITIDGIFEVKATAGDTHLGGEDEDNRLVNH 242
DB 242 YGLDRTGKGERNVLIEDLGSGTFDVSILITIDGIFEVKATAGDTHLGGEDEDNRLVNH 242

```

Db 184 YGLDKGARGQONVLIIFDLGGTDFVSLITLIDDGIFEEVKATAGDTHLGGEDFDNRMVNHFV 243  
QY 243 EEFRRKKKKDIQONKRAVRRLPTACERAKRTLSSSTOASLEIDSLFEGIDFYSITPARF 302  
Db 244 EEFRRKKKKDIQONKRALRLTACDRAKRTLSSSSQASLEIDSLFEGIDFYTATPARF 303  
QY 303 EELCSDLFRSTLEBEVKALRDALDKAQHIDLVLVGGSTRIPKVQKLLQDFNGRDLNKS 362  
Db 304 EELCSDLFRSTLEBEVKALRDALDKSQIHEIYLVGGSTRIPKVQKLLQDFNGRDLNKS 363  
QY 363 INPDEAAYGAAYQAALTMGDKSENODLLLDVAPLSLGLTAGVMTALIKRNSIPT 422  
Db 364 INPDEAAYGAAYQAALTMGDKSENODLLLDVAPLSLGLTAGVMTALIKRNTIPT 423  
QY 423 KOTQIFTTYSDNPGVLIQYEGEBRMTKDNLLGRFELSGIPPARGVPOIEVTFDIDA 482  
Db 424 KOTQIFTTYSDNPGVLIQYFEGEBRMTKDNLLGRFELSGIPPARGVPOIEVTFDIDA 483  
QY 483 NGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAKEYKAEDDEVQERYSARNAL 542  
Db 484 NGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAKEYKAEDDEVQERYSARNAL 543  
QY 543 ESYAFNKKSAVEDEGLKGISEADKKVLDKQCEVISLMDANTLAEKDEFEHKRELEQY 602  
Db 544 ESYAFNKKSAVEDEBNYKGISDEDKRTISEKCTQVISMENNOIAEKEEYAFQOKDLEKY 603  
QY 603 CNPILISGLYOGAGPG--PGGF----GAOGPKGSGSGSPTIEVD 641  
Db 604 COPILITKLYOG-GVPGGVPGGMFGSSCGAQRQGGN-SGPTIEVD 647

Search completed: December 4, 2002, 16:42:15  
Job time : 15 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:52:49 : Search time 11 seconds  
(without alignments)  
946.484 Million cell updates/sec

Title: US-09-646-835-1  
Perfect score: 641  
Sequence: 1 MAKAAIGIDLTGTTSCVGV.....FGAQRKGGSGSGPTIEVD 641

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 103943 seqs, 16242309 residues

Word size : 0

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppaa/PCRUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	641	100.0	641	10	US-09-759-010-3
2	168	26.2	168	10	US-09-864-761-36258
3	101	15.8	642	10	US-09-761-534A-10
4	72	11.2	209	10	US-09-761-534A-12
5	71	11.1	137	10	US-09-925-301-1519
6	53	8.3	646	9	US-09-870-759-43
7	53	8.3	646	9	US-09-759-010-4
8	53	8.3	651	9	US-10-108-605-75
9	47	7.3	665	10	US-09-925-302-724
10	23	3.6	637	10	US-09-815-242-12058
11	17	2.7	52	10	US-09-864-761-35578
12	16	2.5	653	10	US-09-759-010-2
13	16	2.5	654	10	US-09-919-172-54
14	15	2.3	183	10	US-09-841-132-301
15	15	2.3	620	10	US-09-815-242-11472
16	15	2.3	660	10	US-09-841-132-446
17	14	2.2	193	10	US-09-864-761-34864
18	14	2.2	625	9	US-09-712-363-162
19	13	2.0	607	10	US-09-815-242-13379

20	13	2.0	607	10	US-09-815-242-13682	Sequence 13682, A
21	13	2.0	609	10	US-09-815-242-10740	Sequence 10740, A
22	13	2.0	610	10	US-09-815-242-55559	Sequence 5559, Ap
23	13	2.0	618	10	US-09-815-242-12567	Sequence 12567, A
24	13	2.0	618	10	US-09-815-242-12970	Sequence 12970, A
25	13	2.0	635	10	US-09-815-242-112909	Sequence 11209, A
26	11	1.7	11	10	US-09-872-832-29	Sequence 29, Appl
27	11	1.7	210	10	US-09-761-534A-8	Sequence 8, Appl1
28	11	1.7	420	10	US-09-761-534A-6	Sequence 6, Appl1
29	11	1.7	637	10	US-09-759-010-1	Sequence 1, Appl1
30	11	1.7	638	10	US-09-815-242-10015	Sequence 10015, A
31	11	1.7	638	10	US-09-815-242-13713	Sequence 13713, A
32	10	1.6	221	10	US-09-864-761-36116	Sequence 36116, A
33	9	1.4	474	10	US-09-864-761-34320	Sequence 34320, A
34	9	1.4	2237	12	US-10-033-026-8	Sequence 8, Appl1
35	9	1.4	2339	12	US-10-033-026-6	Sequence 6, Appl1
36	9	1.4	2343	12	US-10-033-026-4	Sequence 4, Appl1
37	8	1.2	54	10	US-09-880-713A-23	Sequence 23, Appl
38	8	1.2	54	10	US-09-864-761-42619	Sequence 42619, A
39	8	1.2	174	9	US-09-971-536-72	Sequence 72, Appl
40	8	1.2	530	9	US-10-108-605-171	Sequence 171, App
41	8	1.2	623	9	US-10-108-605-125	Sequence 125, App
42	8	1.2	623	9	US-10-108-605-129	Sequence 129, App
43	7	1.1	20	9	US-10-012-756-14	Sequence 14, Appl
44	7	1.1	76	10	US-09-864-761-42162	Sequence 42162, A
45	7	1.1	123	9	US-09-764-868-925	Sequence 925, App

ALIGNMENTS

RESULT 1  
US-09-759-010-3  
; Sequence 3, Application US/09759010  
; Patent No. US20010034042A1  
; GENERAL INFORMATION:  
; APPLICANT: Sriwastava, Pramod K.  
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK  
; FILE REFERENCE: 8449-135  
; CURRENT APPLICATION NUMBER: US/09/759,010  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 641  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-759-010-3

Query Match	100.0%	Score 641:	DB 10:	Length 641:
Best Local Similarity	100.0%	Pred. No. 0:		
Matches 641:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
Qy	1	MAKAAIGIDLTGTTSCVGVFOHGVKVELIANDQGRTPSYVAFTDRLTGDAKNQYA	60	
Db	1	MAKAAIGIDLTGTTSCVGVFOHGVKVELIANDQGRTPSYVAFTDRLTGDAKNQYA	60	
Qy	61	LNPOVTVDANKRLIGRKGDPVVOGDMKHPFOVINDGDKPVOGYSYGETKAFYPEETS	120	
Db	61	LNPOVTVDANKRLIGRKGDPVVOGDMKHPFOVINDGDKPVOGYSYGETKAFYPEETS	120	
Qy	121	SMVLTAKMEIEAVYGYPTVNAVITVPAYFPNDROKATKDGAVIAGLWLRINEPTAA	180	
Db	121	SMVLTAKMEIEAVYGYPTVNAVITVPAYFPNDROKATKDGAVIAGLWLRINEPTAA	180	
Qy	181	IAYGDRTPGKGRNVLIDLGSGTDFVSLITIDDSIEFVKATAGDTHGGEFQURLVNH	240	
Db	181	IAYGDRTPGKGRNVLIDLGSGTDFVSLITIDDSIEFVKATAGDTHGGEFQURLVNH	240	
Qy	241	FVEEFKRRKKKDISONKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFYISITRA	300	
Db	241	FVEEFKRRKKKDISONKRAVRRLRTACERAKRTLSSTQASLEIDSLFEGIDFYISITRA	300	

```
QY 301 REEELCSDFRSTLEFEKALRDPAKIDKQAQIHDLVVGSGSTRIPKVOKLLDFFNGRDIN 360
    |||||||
Db 301 REEELCSDFRSTLEFEKALRDPAKIDKQAQIHDLVVGSGSTRIPKVOKLLDFFNGRDIN 360
QY 361 KSIINPEAAVAGAAVQAALIMGDKSENVDLLLDVAPLSLGLTGAAGWTALIKRNSIT 420
    |||||||
Db 361 KSIINPEAAVAGAAVQAALIMGDKSENVDLLLDVAPLSLGLTGAAGWTALIKRNSIT 420
QY 421 PRKQTOIFFTYSNPGVLIQVYEGERAMTKDNNLGRFELSITPAPRGVPOIEVTFPI 480
    |||||||
Db 421 PRKQTOIFFTYSNPGVLIQVYEGERAMTKDNNLGRFELSITPAPRGVPOIEVTFPI 480
QY 481 DANGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYKAEDVOERYSARN 540
    |||||||
Db 481 DANGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYKAEDVOERYSARN 540
QY 541 ALESYAFNNKSAVEDGLGKISADKKVLDKCEVISMLANTLAEKDEPHKKELE 600
    |||||||
Db 541 ALESYAFNNKSAVEDGLGKISADKKVLDKCEVISMLANTLAEKDEPHKKELE 600
QY 601 QVCNPIISGLYOGAGGPGGFGAGCPKGSAGSGPTIEVD 641
    |||||||
Db 601 QVCNPIISGLYOGAGGPGGFGAGCPKGSAGSGPTIEVD 641
```

```
RESULT 2
US-09-864-761-36258
; Sequence 36258, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
```

```
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36258
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF134726.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 87
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
; OTHER INFORMATION: SWISSPROT HIT: P08107, EVALUATE 1.00e-74
; OTHER INFORMATION: EST_HUMAN HIT: A132959.1, EVALUATE 8.00e-74
US-09-864-761-36258
```

```
Query Match 26.2%; Score 168; DB 10; Length 168;
Best Local Similarity 100.0%; Pred. No. 8.7e-152;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 474 IEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYKAEDVOR 533
    |||||||
Db 1 IEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEIERMVOEAKRYKAEDVOR 60
QY 534 EYVSAKNALESYAFNNKSAVEDGLGKISADKKVLDKCEVISMLANTLAEKDEPH 593
    |||||||
Db 61 EYVSAKNALESYAFNNKSAVEDGLGKISADKKVLDKCEVISMLANTLAEKDEPH 120
QY 594 HRRKELEQVCNPIISGLYOGAGGPGGFGAGCPKGSAGSGPTIEVD 641
    |||||||
Db 121 HRRKELEQVCNPIISGLYOGAGGPGGFGAGCPKGSAGSGPTIEVD 168
```

```
RESULT 3
US-09-761-534A-10
; Sequence 10, Application US/09761534A
; Patent No. US20020146426A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Palliser, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eisen, Herman N.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/09/761,534A
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hap70
US-09-761-534A-10
```

Query Match 15.8%; Score 101; DB 10; Length 642;  
Best Local Similarity 100.0%; Pred. No. 9.7e-88;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 PVTAAVITVPAYFNDSDQRAKDGAVIAGLVLRITINEPTAAIAVGLDRTGKGERNVLT 197  
|||||  
DB 138 PVTAAVITVPAYFNDSDQRAKDGAVIAGLVLRITINEPTAAIAVGLDRTGKGERNVLT 197  
|||||

QY 198 FDLGGGTFDVSILTIIDGIFEVKATAGCTHLGGEDEPNRLV 238  
|||||  
DB 198 FDLGGGTFDVSILTIIDGIFEVKATAGCTHLGGEDEPNRLV 238  
|||||

RESULT 4  
US-09-761-534A-12  
; Sequence 12, Application US/09761534A  
; Patent No. US20020146426A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Qian  
; APPLICANT: Richmond, Joan F.L.  
; APPLICANT: Cho, Bryan K.  
; APPLICANT: Palliser, Deborah  
; APPLICANT: Chen, Jianzhu  
; APPLICANT: Eisen, Herman N.  
; APPLICANT: Young, Richard A.  
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock  
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and Is  
; FILE REFERENCE: CD4-T-Cell-Independent  
; CURRENT APPLICATION NUMBER: US/09/761,534A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: PCT/US00/32831  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/176,143  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Murine hsp70 - Segment II  
US-09-761-534A-12

Query Match 11.2%; Score 72; DB 10; Length 209;  
Best Local Similarity 100.0%; Pred. No. 1.1e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 HVEFEKRRKKKDISONKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFTTSTR 299  
|||||  
DB 51 HVEFEKRRKKKDISONKRAVRRLTACERAKRTLSSTQASLEIDSLFEGIDFTTSTR 110  
|||||

QY 300 ARFELCSDLFR 311  
|||||  
DB 111 ARFELCSDLFR 122  
|||||

RESULT 5  
US-09-925-301-1519  
; Sequence 1519, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; PRIOR FILING DATE: 2001-08-10  
; CURRENT APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1519  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (72)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-301-1519

Query Match 11.1%; Score 71; DB 10; Length 137;  
Best Local Similarity 100.0%; Pred. No. 6.9e-60;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 DSQRAKRDAGVIAGLVLRITINEPTAAIAVGLDRTGKGERNVLPDLGGGTFDVSILT 211  
|||||  
DB 1 DSQRAKRDAGVIAGLVLRITINEPTAAIAVGLDRTGKGERNVLPDLGGGTFDVSILT 60  
|||||

QY 212 IDDGIFEVKAT 222  
|||||  
DB 61 IDDGIFEVKAT 71  
|||||

RESULT 6  
US-09-870-759-43  
; Sequence 43, Application US/09870759  
; Patent No. US20020177551A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 870759  
; CURRENT APPLICATION NUMBER: US/09/870,759  
; PRIOR FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 60/208,128  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 43  
; LENGTH: 646  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-870-759-43

Query Match 8.3%; Score 53; DB 9; Length 646;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GIDGTTSCVGVFQHGKVEIITANDGNNRTTPSYAFTDTERLTIGDAKNQVA 60  
|||||  
DB 8 GIDGTTSCVGVFQHGKVEIITANDGNNRTTPSYAFTDTERLTIGDAKNQVA 60  
|||||

RESULT 7  
US-09-759-010-4  
; Sequence 4, Application US/09759010  
; Patent No. US20010034042A1  
; GENERAL INFORMATION:  
; APPLICANT: Srivastava, Pramod K.  
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK  
; FILE REFERENCE: 8449-135  
; CURRENT APPLICATION NUMBER: US/09/759,010  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 646  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-759-010-4

Query Match 8.3%; Score 53; DB 10; Length 646;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GIDLGTTCVGVFQHGKVEIILANDGNNRTTPTSYVAFDTERLIGDAKNOVA 60  
DB 8 GIDLGTTCVGVFQHGKVEIILANDGNNRTTPTSYVAFDTERLIGDAKNOVA 60

## RESULT 8

US-10-108-605-75  
; Sequence 75, Application US/10108605  
; Patent No. US20020160934A1  
; GENERAL INFORMATION:  
; APPLICANT: Broadus, Julie  
; APPLICANT: Stam, Lynn  
; APPLICANT: Bachmann, Jane  
; APPLICANT: Kamdar, Kim  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE  
; FILE REFERENCE: 3113B  
; CURRENT APPLICATION NUMBER: US/10/108,605  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US 09/761,142  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/176,418  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 75  
; LENGTH: 651  
; TYPE: PRF  
; ORGANISM: Drosophila melanogaster  
US-10-108-605-75

Query Match 8.3%; Score 53; DB 9; Length 651;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GIDLGTTCVGVFQHGKVEIILANDGNNRTTPTSYVAFDTERLIGDAKNOVA 60  
DB 8 GIDLGTTCVGVFQHGKVEIILANDGNNRTTPTSYVAFDTERLIGDAKNOVA 60

## RESULT 9

US-09-925-302-724  
; Sequence 724, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 724  
; LENGTH: 665  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
; PEATURE:  
; NAME/KEY: SITE  
; LOCATION: (216)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (298)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-302-724

Query Match 7.3%; Score 47; DB 10; Length 665;  
Best Local Similarity 100.0%; Pred. No. 1.6e-36;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 440 IQVYEGERAMTKDNNLGRFELSGTPAPRGVQIETVDIDANGIL 486  
DB 464 IQVYEGERAMTKDNNLGRFELSGTPAPRGVQIETVDIDANGIL 510

## RESULT 10

US-09-815-242-12058  
; Sequence 12058, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12058  
; LENGTH: 637  
; TYPE: PRF  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-12058

Query Match 3.6%; Score 23; DB 10; Length 637;  
Best Local Similarity 100.0%; Pred. No. 8.9e-14;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 IPPAPRGVQIETVDIDANGIL 486  
DB 462 IPPAPRGVQIETVDIDANGIL 484

## RESULT 11

US-09-864-761-35578  
; Sequence 35578, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; FILE REFERENCE: Aecomics-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312



```
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35578
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009945.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 54
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 45
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 33
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.9
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 89
; OTHER INFORMATION: SWISSPROT HIT: P08109, EVALUATE 5.00e-22
; OTHER INFORMATION: EST_HUMAN HIT: BF212199.1, EVALUATE 7.00e-21
US-09-864-761-35578

Query Match          2.7%; Score 17; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 470 GVPQIEVTFDIDANGIL 486
Db 29 GVPQIEVTFDIDANGIL 45

RESULT 12
US-09-759-010-2
; Sequence 2, Application US/09759010
; Patent No. US20010034042A1
; GENERAL INFORMATION:
; APPLICANT: Srivastava, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
```

```
; TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
; FILE REFERENCE: 8449-135
; CURRENT APPLICATION NUMBER: US/09/759,010
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-010-2

Query Match          2.5%; Score 16; DB 10; Length 653;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 171 RIINEPTAAAIAYGLD 186
Db 197 RIINEPTAAAIAYGLD 212

RESULT 13
US-09-919-172-54
; Sequence 54, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Fatis, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 2993696CD1
US-09-919-172-54

Query Match          2.5%; Score 16; DB 10; Length 654;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 171 RIINEPTAAAIAYGLD 186
Db 197 RIINEPTAAAIAYGLD 212

RESULT 14
US-09-841-132-301
; Sequence 301, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 301
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Chlamydia
```

US-09-841-132-301

Query Match 2.3%; Score 15; DB 10; Length 183;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 472 PQIEVTFDIDANGIL 486  
|||||  
Db 9 PQIEVTFDIDANGIL 23

RESULT 15

US-09-815-242-11472  
; Sequence 11472, Application US/09815242  
; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11472

; LENGTH: 620

; TYPE: PRT

; ORGANISM: Helicobacter pylori

US-09-815-242-11472

Query Match 2.3%; Score 15; DB 10; Length 620;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 472 PQIEVTFDIDANGIL 486  
|||||  
Db 464 PQIEVTFDIDANGIL 478

Search completed: December 4, 2002, 16:56:53  
Job time : 12 secs

>gi|347019|pir||S31716 dnaK-type molecular chaperone hsp72-ps1 - rat  
 gi|56385|emb|CAA49670.1| Hsc70-ps1 [Rattus norvegicus]  
 Length = 646

Score = 505 bits (1301), Expect = e-142  
 Identities = 259/328 (78%), Positives = 288/328 (87%)

Query: 1 IDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDVLVLVGGSTRI 60  
 IDSL+EGIDFYTSITRARFEEL +DLFR TL+PVEKALRDAKLDK+QIHD+VLVGGSTRI  
 Sbjct: 284 IDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAKLDKSQIHDIVLVGGSTRI 343

Query: 61 PKVQKLLQDFFNGRDNLNKSINPDEXXXXXXXXXXXXXILMGDKSENVQDXXXXXXXXXXXXX 120  
 PK+QKLLQDFFNG++LNKSINPDE IL GDKSENVQD  
 Sbjct: 344 PKIQKLLQDFFNGKELNKSINPDEAVAYGA AVQAAILSGDKSENVQDLLLLDVTPLSLGI 403

Query: 121 ETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSG 180  
 ETAGGVMT LIKRN+TIPTKQTQ FTTYSDNQPGVLIQVYEGERAMTKDNNLLG+FEL+G  
 Sbjct: 404 ETAGGVMTVLIKRNTTIPTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTG 463

Query: 181 IPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAE 240  
 IPPAPRGVPQIEVTFDIDANGILNV+A DKSTGK NKITITNDKGRLSKE+IERMVQEAE  
 Sbjct: 464 IPPAPRGVPQIEVTFDIDANGILNVS AVDKSTGKENKITITNDKGRLSKEDIERMVQEAE 523

Query: 241 KYKAEDEVQRERVS AKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDA 300  
 KYKAEDE QR++VS+KN+LESYAFNMK+ VEDE L+GKI++ DK+K+LDKC E+ISWLD  
 Sbjct: 524 KYKAEDEKQRDKVSSKNSLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIISWLDK 583

Query: 301 NTLAEKDEFEHKRKELEQVCNPIISGLY 328  
 N AEK+EFEH++KELE+VCNPII+ LY  
 Sbjct: 584 NQTAEKEEFEHQKELEKVCNPIITKLY 611

**THIS PAGE BLANK (USPTO)**